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From: Saidha, Tekchand
Sent: Thursday, July 24, 2003 10:35 AM
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Subject: 09/663481

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09/663481

Please search the data bases and interference files for _

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Tekchand Saidha
Primary Examiner
Art Unit 1652, CM1, Room No. 10D05
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(703) 305-6595

Searcher: M. Smith
Phone: _____
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Date Picked Up: 7/30 - 8/1/03
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TYPE OF SEARCH:
NA Sequences: 1
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Structures: _____
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 10, 2003, 22:28:01 ; Search time 73 Seconds
(without alignments)
1121.958 Million cell updates/sec

Title: US-09-663-481-1

Perfect score: 2676

Sequence: 1 MANFVPVQRSLQGLILRLR.....EEAPPSPAEDHNQNGNLD 516

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_19Jun03.*

1: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
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22: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2676	100.0	516	22 AAB35470	Human cyclic nucle
2	2582	96.5	536	20 AAW95110	Human RPMI 8392 ce
3	2484.5	92.8	534	16 AARG9720	Cyclic-GMP stimula
4	2484.5	92.8	534	18 AAW18038	Bovine brain 63 kD
5	2484.5	92.8	534	18 AAW11251	63 kD calcium/cal
6	2484.5	92.8	534	19 AAW77039	Bovine brain Ca2+/
7	2484.5	92.8	534	19 AAW71223	63 kDa Cam-PDE enc
8	2484.5	92.8	534	19 AAW60751	63 kDa bovine Cam-
9	2484.5	92.8	534	21 AAY80977	Bovine brain 63 kD

10	2484.5	92.8	534	24 AAB58716	Bovine brain 63kDa
11	2478.5	92.6	534	13 AAR28404	63 kD Cam PDE from
12	1636.5	61.2	514	16 AARG9715	Cyclic-GMP stimula
13	1636.5	61.2	514	18 AAW18037	Bovine lung 59 kDa
14	1636.5	61.2	514	18 AAW11240	Calcium/calmodulin
15	1636.5	61.2	514	19 AAW77037	Bovine lung Ca2+/c
16	1636.5	61.2	514	19 AAW71221	59 kDa Cam-PDE fro
17	1636.5	61.2	514	19 AAW60749	59 kDa bovine Cam-
18	1636.5	61.2	514	21 AAY80972	Bovine lung 59 kD
19	1636.5	61.2	514	24 AAB58711	Bovine heart full
20	1633.5	61.0	514	13 AAR28401	Bovine lung 59 kD
21	1593	59.5	634	16 AARG9732	Cyclic-GMP stimula
22	1593	59.5	634	18 AAW18040	Human brain 61 kDa
23	1593	59.5	634	18 AAW11256	Hippocampus calcu
24	1593	59.5	634	19 AAW71228	Human 61 kDa Cam-P
25	1593	59.5	634	19 AAW77044	Ca2+/calmodulin st
26	1593	59.5	634	19 AAW60756	Amino acid sequenc
27	1593	59.5	634	21 AAY80989	Human 61 kD Cam-PD
28	1593	59.5	634	24 AAB58728	Human 61kDa Cam-PD
29	1591.5	59.5	530	16 AARG9711	Cyclic-GMP stimula
30	1591.5	59.5	530	18 AAW18036	Bovine brain 61 kD
31	1591.5	59.5	530	18 AAW11243	61 kD brain calcu
32	1591.5	59.5	530	19 AAW77036	Bovine brain Ca2+/
33	1591.5	59.5	530	19 AAW71220	61 kDa Cam-PDE DNA
34	1591.5	59.5	530	19 AAW60747	Hippocampus calcu
35	1591.5	59.5	530	21 AAY80968	Bovine brain 61 kD
36	1591.5	59.5	530	24 AAB58707	Bovine brain full
37	1589.5	59.4	530	13 AAR28395	Bovine brain Cam P
38	1576	58.9	634	13 AAR28412	Prod. cDNA insert
39	1568.5	58.6	535	16 AARG9731	Cyclic-GMP stimula
40	1568.5	58.6	535	18 AAW18039	Human brain 61 kDa
41	1568.5	58.6	535	18 AAW11255	Hippocampus calcu
42	1568.5	58.6	535	19 AAW71227	Human 61 kDa Cam-P
43	1568.5	58.6	535	19 AAW77043	Human Ca2+/calmodu
44	1568.5	58.6	535	19 AAW60755	Amino acid sequenc
45	1568.5	58.6	535	21 AAY80988	Human 61 kD Cam-PD

ALIGNMENTS

RESULT 1

AAB35470
ID AAB35470 standard; protein; 516 AA.

AC AAB35470;

DT 06-JUN-2001 (first entry)

XX Human cyclic nucleic acid phosphodiesterase PDE1B2.

DE Human; cyclic nucleic acid phosphodiesterase; PDE1B2; spleen;
KW cardiovascular disease; gastrointestinal disorder; sexual dysfunction.

XX Homo sapiens.

PN EP1085092-A1.

XX 21-MAR-2001.

PF 14-SEP-2000; 2000EP-0307982.

XX 17-SEP-1999; 99GB-0022125.

XX (PFIZ) PFIZER LTD.

PA (PFIZ) PFIZER INC.

PI Fidock MD;

XX WPI; 2001-246901/26.

DR N-PSDB; AAF62301.

XX Human cyclic nucleotide phosphodiesterase 1B2 and its nucleotide

PT sequence useful for treating cardiovascular, gastrointestinal and
 PT spleen disorders and screening for drugs to treat associated disorders

XX Claim 1; Page 42-45; 58pp; English.

XX The present invention provides the protein and coding sequences for the
 CC human cyclic nucleic acid phosphodiesterase PDE1B2. This is thought to be
 CC a splice variant of PDE1, and capable of catalyzing the degradation of
 CC cAMP and/or cGMP. The sequences are useful in the treatment of
 CC cardiovascular, gastrointestinal and spleen disorders, and in the
 CC enhancement of the male erectile response and treatment of female sexual
 CC dysfunction. The present sequence is the PDE1B2 protein.

XX Sequence 516 AA;

Query Match 100.0%; Score 2676; DB 22; Length 516;
 Best Local Similarity 100.0%; Pred. No. 7, 4e-245;
 Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANPVPQVSHLOGPTILRLRYMVKOLENGEINIEELKKNLEYTASLLEAVYIDETROIID 60

DB 1 MANPVPQVSHLOGPTILRLRYMVKOLENGEINIEELKKNLEYTASLLEAVYIDETROIID 60

QY 61 TEDELQELSDAVSEVROWLASTFTQOARAKGRRAEERPKFRSIVHAVQAGIFYVERMR 120

DB 61 TEDELQELSDAVSEVROWLASTFTQOARAKGRRAEERPKFRSIVHAVQAGIFYVERMR 120

QY 121 RYTSVGPYSTAVLNCLNLDWCDFVSLNQAADHALRTIVFELLRNHLISRFKIP 180

DB 121 RYTSVGPYSTAVLNCLNLDWCDFVSLNQAADHALRTIVFELLRNHLISRFKIP 180

QY 181 TVFLMSFLDALETGYKYNPNYHQAADVTQVHCFLIRGTGMVHCLSEIELLAIIFAA 240

DB 181 TVFLMSFLDALETGYKYNPNYHQAADVTQVHCFLIRGTGMVHCLSEIELLAIIFAA 240

QY 241 AIHDYHTGTNFSHIOKSECAIVYNDRSVLENHHISSVFRMQDDNMNIFINTKDEF 300

DB 241 AIHDYHTGTNFSHIOKSECAIVYNDRSVLENHHISSVFRMQDDNMNIFINTKDEF 300

QY 301 VELRALVIEMLVLTMSCHFPQVKTKMTALQQLERIDKPKALSLLHAADISHPTKQWLV 360

DB 301 VELRALVIEMLVLTMSCHFPQVKTKMTALQQLERIDKPKALSLLHAADISHPTKQWLV 360

QY 361 HSRWTKALMBEFPFGDKEAELGLPSPICDRTSTLVAQSQIGFIDFIVEPTFSVLTDVA 420

DB 361 HSRWTKALMBEFPFGDKEAELGLPSPICDRTSTLVAQSQIGFIDFIVEPTFSVLTDVA 420

QY 421 EKSVPQPLADEDSKKNQPSQFOWRPSLDVEGDPNDVVSFRSTWVKRIQENKQWKERA 480

DB 421 EKSVPQPLADEDSKKNQPSQFOWRPSLDVEGDPNDVVSFRSTWVKRIQENKQWKERA 480

QY 481 ASGITNOMSIDELSPCEEAPPSPADEHNQNGND 516

DB 481 ASGITNOMSIDELSPCEEAPPSPADEHNQNGND 516

RESULT 2

AAW95110 standard; Protein; 536 AA.

XX AC AAW95110;

XX DT 26-MAY-1999 (first entry)

XX Human RPMI-8392 cell phosphodiesterase, PDE1B1.

XX Antisense oligodeoxynucleotide; phosphodiesterase; PDE1B1; enzyme; PDE;

XX cell death; apoptosis; cancer; Ca2+-calmodulin; lymphoblastoid; RNase H;

XX RPMI 8392; RNA degradation; CAMP; immunoproliferative disorder; breast;

XX Immune dysfunction; acute lympholytic leukemia; prostate; human.

XX Homo sapiens.

OS

XX US585834-A.

XX 23-MAR-1999.

XX 30-SEP-1997.

XX 30-SEP-1996;

XX 30-SEP-1997;

XX (EPST/) EPSTEIN P M.

XX Epstein PM;

XX WPI; 1999-228548/19.

XX N-PSDB; AAX26288.

XX Antisense oligodeoxynucleotides specific for mRNA encoding
 PT phosphodiesterase PDE1B1 enzymes and method for using them to induce
 PT apoptosis of cells - useful in the treatment of immunoproliferative
 PT disorders and immune dysfunctions

XX Disclosure; Fig 8A-D; 35pp; English.

XX The invention relates to antisense oligodeoxynucleotides (AS-ODN) which
 CC will bind to mRNA encoding phosphodiesterase PDE1B1 enzymes and their use
 CC in inducing programmed cell death (apoptosis) in cancer cells. PDE1 is a
 CC Ca2+-calmodulin dependent phosphodiesterase found in cytosolic extracts
 CC of human lymphoblastoid cell line, RPMI 8392. The method in which
 CC programmed cell death is induced in cancer cells comprises: (1)
 CC identifying the phosphodiesterase enzyme PDE1B1 in a cell line containing
 CC the cancer cells; (2) synthesizing an AS-ODN inhibitor which will bind to
 CC mRNA encoding PDE1B1; and (3) applying the AS-ODN to the cell line to
 CC inhibit the enzymatic activity of the PDE1B1 and induce apoptosis in the
 CC cells. The AS-ODNs inhibit the expression of a protein by two mechanisms:
 CC (i) by degradation of RNA by the ubiquitous enzyme RNase H, which
 CC selectively cleaves the RNA of DNA-RNA heteroduplexes; and (ii) the
 CC arrest of translation initiation caused by AS-ODN hybridization to the 5'
 CC un-translated region or the translation initiation site on the mRNA.
 CC Inhibition of phosphodiesterase (PDE) enzyme expression results in
 CC elevated levels of cAMP in the cells due to PDE1B1 being involved in the
 CC metabolism of cAMP. The elevated cAMP levels result in apoptosis by
 CC inhibition of DNA synthesis. The method and AS-ODN are useful in inducing
 CC cAMP stimulated apoptosis and in the treatment of immunoproliferative
 CC disorders and immune dysfunctions such as acute lympholytic leukemia,
 CC breast and prostate cancer. The present sequence represents a human RPMI
 CC 8392 cell PDE1B1.

XX Sequence 536 AA;

Query Match 96.5%; Score 2582; DB 20; Length 536;
 Best Local Similarity 100.0%; Pred. No. 6, 5e-236;
 Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 LRYMVKOLENGEINIEELKKNLEYTASLLEAVYIDETROIIDTEDELQELSDAVSEVR 78

DB 19 LRYMVKOLENGEINIEELKKNLEYTASLLEAVYIDETROIIDTEDELQELSDAVSEVR 78

QY 39 LRYMVKOLENGEINIEELKKNLEYTASLLEAVYIDETROIIDTEDELQELSDAVSEVR 98

DB 39 LRYMVKOLENGEINIEELKKNLEYTASLLEAVYIDETROIIDTEDELQELSDAVSEVR 98

QY 79 DMLASTFTQOARAKGRRAEERPKFRSIVHAVQAGIFYVERMRRTYTSVGPYSTAVLNCL 138

DB 79 DMLASTFTQOARAKGRRAEERPKFRSIVHAVQAGIFYVERMRRTYTSVGPYSTAVLNCL 138

QY 99 DMLASTFTQOARAKGRRAEERPKFRSIVHAVQAGIFYVERMRRTYTSVGPYSTAVLNCL 158

DB 99 DMLASTFTQOARAKGRRAEERPKFRSIVHAVQAGIFYVERMRRTYTSVGPYSTAVLNCL 158

QY 139 KNLDLWCDFVSLNQAADHALRTIVFELLRNHLISRFKIPFVFLMSFLDALETGYGKY 198

DB 139 KNLDLWCDFVSLNQAADHALRTIVFELLRNHLISRFKIPFVFLMSFLDALETGYGKY 198

QY 159 KNLDLWCDFVSLNQAADHALRTIVFELLRNHLISRFKIPFVFLMSFLDALETGYGKY 218

DB 159 KNLDLWCDFVSLNQAADHALRTIVFELLRNHLISRFKIPFVFLMSFLDALETGYGKY 218

QY 199 KNPYHQAADVTQVHCFLIRGTGMVHCLSEIELLAIIFAAAIHDYHTGTNFSHIOK 258

DB 199 KNPYHQAADVTQVHCFLIRGTGMVHCLSEIELLAIIFAAAIHDYHTGTNFSHIOK 258

QY 219 KNPYHQAADVTQVHCFLIRGTGMVHCLSEIELLAIIFAAAIHDYHTGTNFSHIOK 278

DB 219 KNPYHQAADVTQVHCFLIRGTGMVHCLSEIELLAIIFAAAIHDYHTGTNFSHIOK 278

QY 259 KSECAIVYNDRSVLENHHISSVFRMQDDNMNIFINTKDEFVEKRALVIEMLVLTMSCH 318

DB 259 KSECAIVYNDRSVLENHHISSVFRMQDDNMNIFINTKDEFVEKRALVIEMLVLTMSCH 318

OS 279 KSECAIVYNDRSVLENHHISSVFRMQDDNMNIFINTKDEFVEKRALVIEMLVLTMSCH 338

QY 319 HFQVQTKMTALQQLERIDKPKALSLLLHAADISHPTKQWLHVSRTWKALMEEFFRQGD 378
DB 339 HFQVQTKMTALQQLERIDKPKALSLLLHAADISHPTKQWLHVSRTWKALMEEFFRQGD 398
QY 379 EAEGLPFPSPCLDRSTLVAQSQIGFIDIVEPTFSLTDVAEKSVQPLADEDSKKNOP 438
DB 399 EAEGLPFPSPCLDRSTLVAQSQIGFIDIVEPTFSLTDVAEKSVQPLADEDSKKNOP 458
QY 439 SFQWQPSLDVEGDPNDVFSRSTWVKRIQENKOKWKERAASGITNOMSIDELSPCEE 498
DB 459 SFQWQPSLDVEGDPNDVFSRSTWVKRIQENKOKWKERAASGITNOMSIDELSPCEE 518
QY 499 EAPPSPAEDEHNGNGLD 516
DB 519 EAPPSPAEDEHNGNGLD 536

RESULT 3
AAR69720
ID AAR69720 standard; Protein: 534 AA.

XX AAR69720;

XX 25-MAR-2003 (updated)

DT 11-OCT-1995 (first entry)

XX Cyclic-GMP stimulated nucleotide PDE clone p12-3a.

DE Cyclic-GMP stimulated nucleotide phosphodiesterase;

KW bovine brain; hormones; neurotransmitters; transmission regulation;

KW antibodies; enzyme purification; clone p12-3a.

XX Bos taurus.

XX US5389527-A.

XX 14-FEB-1995.

PF 20-APR-1992; 92US-0872644.

PR 19-APR-1991; 91US-0688356.

PR 20-APR-1992; 92US-0872644.

XX (UNIW) UNIV WASHINGTON.

Beavo JA, Charbonneau H, Sonnenburg WK;

WPI; 1995-090205/12.

DR N-PSDB; AAQ83969.

XX New nucleic acid encoding cyclic-GMP stimulated nucleotide

PT phosphodiesterase - and related vectors and transformed cells,

PT useful for screening cpds. for phosphodiesterase modulating

PT activity

XX Example 3; Columns 55-60; 69pp; English.

PS AAQ83969 encodes AAR69720 the bovine brain cyclic-GMP stimulated

CC nucleotide phosphodiesterase (Cam PDE) clone p12.3a. Eukaryotic cells

CC that express Cam PDE can be used to screen cpds. for the ability to

CC modulate Cam PDE activity. Cam PDEs are involved in regulating

CC the transmission of information from hormones, neurotransmitters

CC or other systems that use cyclic nucleotides as messengers.

CC Antibodies raised against Cam PDE can be used for enzyme purificn.,

QY 19 LRYMVKQLENGEINIEELKKNLEYTASLEAVYIDETROILDELOELRSDAVPSEVR 78
DB 38 LRYMVKQLENGEINIEELKKNLEYTASLEAVYIDETROILDELOELRSDAVPSEVR 97
QY 79 DWLASTFTQOARAKARRAEKPKRSIVHAVAQAGIFVERMFRRTYTSVGPPTYSTAVLNCL 138
DB 98 DWLASTFTQOARAKARRAEKPKRSIVHAVAQAGIFVERMFRRTYTSVGPPTYSTAVLNCL 156
QY 139 KNLDLWCDFVFSINQAADHALRTIVFELLTRHNLISREKIPVFLMFLSFLDALETGYGY 198
DB 157 KNLDLWCDFVFSINQAADHALRTIVFELLTRHNLISREKIPVFLMFLSFLDALETGYGY 216
QY 199 KNPYHNOIHAADVOTVHCFLRTGMVHCLSEIELLAIIFAAAIHDYEHTGTNSPHIQ 258
DB 217 KNPYHNOIHAADVOTVHCFLRTGMVHCLSEIELLAIIFAAAIHDYEHTGTNSPHIQ 276
QY 259 KSECAIVYNDRSVLENNHISVFRMLQDDMMNIFNLTKDEFVELRALVIEVWLATDMSC 318
DB 277 KSECAIVYNDRSVLENNHISVFRMLQDDMMNIFNLTKDEFVELRALVIEVWLATDMSC 336
QY 319 HFQVQTKMTALQQLERIDKPKALSLLLHAADISHPTKQWLHVSRTWKALMEEFFRQGD 378
DB 337 HFQVQTKMTALQQLERIDKPKALSLLLHAADISHPTKQWLHVSRTWKALMEEFFRQGD 396
QY 379 EAEGLPFPSPCLDRSTLVAQSQIGFIDIVEPTFSLTDVAEKSVQPLADEDSKKNOP 438
DB 397 EAEGLPFPSPCLDRSTLVAQSQIGFIDIVEPTFSLTDVAEKSVQPLADEDSKKNOP 456
QY 439 SFQWQPSLDVEGDPNDVFSRSTWVKRIQENKOKWKERAASGITNOMSIDELSPCEE 498
DB 457 SFQWQPSLDVEGDPNDVFSRSTWVKRIQENKOKWKERAASGITNOMSIDELSPCEE 516
QY 499 EAPPSPAEDEHNGNGLD 516
DB 517 EAPPSPAEDEHNGNGLD 534

RESULT 4

AAW18038

ID AAW18038 standard; protein: 534 AA.

XX AC AAW18038;

XX 25-MAR-2003 (updated)

DT 31-JUL-1997 (first entry)

XX Bovine brain 63 kDa Ca2+/calmodulin stimulated phosphodiesterase.

XX Ca2+/calmodulin stimulated cyclic nucleotide phosphodiesterase enzyme;

XX calcium ion; Cam-PDE; antibody; cow.

XX Bos taurus.

XX US5602019-A

XX 11-FEB-1997.

XX 29-AUG-1994; 94US-0297510.

XX 20-APR-1992; 92US-0872644.

XX 19-APR-1991; 91US-0688356.

XX 29-AUG-1994; 94US-0297510.

XX (UNIW) UNIV WASHINGTON.

XX Sonnenburg WK, Charbonneau H, Bentley JK, Beavo JA;

XX WPI; 1997-131799/12.

XX N-PSDB; AAT67200.

XX DNA encoding bovine and human phosphodiesterase enzymes - stimulated

PT by calcium/calmodulin, useful for recombinant prodn. of the enzymes

Query Match 92.88; Score 2484.5; DB 16; Length 534;

Best Local Similarity 96.0%; Pred. No. 1.2e-226;

Matches 478; Conservative 10; Mismatches 9; Indels 1; Gaps 1;

CC catalyse the hydrolysis of cyclic nucleotides and as such control their
 CC intracellular level, they are controlled by second messengers e.g. Ca2+
 CC and calmodulin and transmembrane signals and through pathways involving
 CC these, regulate flow of information from extracellular hormones,
 CC neurotransmitters and other signals using cyclic nucleotides as
 CC messengers. The specification describes an assay for identifying a
 CC chemical agent which modifies the enzymatic activity of a mammalian
 CC Cam-PDE. The assays are useful for identifying modulators of Cam-PDEs.
 CC The assay is carried out by incubating cells expressing Cam-PDE with the
 CC suspected modulator and measuring its effect e.g. monitoring the
 CC hydrolysis of cAMP and/or cGMP.

XX Sequence 534 AA;
 Query Match 92.8%; Score 2484.5; DB 19; Length 534;
 Best Local Similarity 96.0%; Pred. No. 1.2e-226;
 Matches 478; Conservative 10; Mismatches 9; Indels 1; Gaps 1;
 QY 19 LRYMVKQLENGEINIEELKKNLEYTASLLEAVYIDETROILDELOELRSDAVPSEVR 78
 DB 38 LRYMVKQLENGEINIEELKKNLEYTASLLEAVYIDETROILDELOELRSDAVPSEVR 97
 QY 79 DWLASTFTQOARAKGRRAEKPFRSIVHAVQAGIFVERMFRRTYTSVGPSTAVLNCL 138
 DB 98 DWLASTFTQOARAKGRRAEKPFRSIVHAVQAGIFVERMFRRTYTSVGPSTAVLNCL 156
 QY 139 KNLDLWCFDVSFSLNOADDDHALRTIVFELLTRNLISRPKIPVFLMSFLDALETGYGY 198
 DB 157 KNVDLWCFDVSFSLNOADDDHALRTIVFELLTRNLISRPKIPVFLMSFLDALETGYGY 216
 QY 199 KNPYHNOIHAADVTQVHCFLRTGVMVHCLSEIELLAIIFAAAIHDYEHGTGTTNSPHIOT 258
 DB 217 KNPYHNOIHAADVTQVHCFLRTGVMVHCLSEIELLAIIFAAAIHDYEHGTGTTNSPHIOT 276
 QY 259 KSECAIYNDRSVLENHHISSVFRMLQDDMMNIFNLTKDEFVELRALVIEMVLATDMSC 318
 DB 277 KSECAIYNDRSVLENHHISSVFRMLQDDMMNIFNLTKDEFVELRALVIEMVLATDMSC 336
 QY 319 HFQOVKMTALQOQLERIDPKALSLLLHAADISHPTKQWLIVHSRWTKALMEEFPRQGDK 378
 DB 337 HFQOVKMTALQOQLERIDPKALSLLLHAADISHPTKQWLIVHSRWTKALMEEFPRQGDK 396
 QY 379 EAEGLGFPSPCLDRTSTLVAQSQIGFIDFIVEPTFSLTDVAEKSVQPLADEDSKSNOP 438
 DB 397 EAEGLGFPSPCLDRTSTLVAQSQIGFIDFIVEPTFSLTDVAEKSVQPLADEDSKSNOP 456
 QY 439 SFQWRQPSLDVEGDPNPVSPRSTWTKYIQENKQKWKERAAAGITNOMSIDELSPCEE 498
 DB 457 SFQWRQPSLDVEGDPNPVSPRSTWTKYIQENKQKWKERAAAGITNOMSIDELSPCEE 516
 QY 499 EAPPSPAEDHNGNGLD 516
 DB 517 EAPPSPAEDHNGNGLD 534

RESULT 8

AAW60751
 ID AAW60751 standard; Protein; 534 AA.

XX
 AC AAW60751;

XX
 DT 07-SEP-1998 (first entry)

XX
 DE 63 kDa bovine Cam-PDE protein.

XX Bovine; decrease; intracellular concentration; cAMP; cGMP;
 XX calcium ion/calmodulin stimulated cyclic nucleotide phosphodiesterase;
 XX Cam-PDE; therapy; prognosis; diagnosis; specific modulator;
 XX Cam-PDE activity; identification; signalling; extracellular hormone;
 XX neurotransmitter; selective inhibitor; cardiotoxic; antidepressant;
 XX antihypertensive; antithrombotic agent.

OS Bos sp.

XX US5776752-A.
 PN 07-JUL-1998.
 PD 07-JUN-1995; 95US-0479532.
 PF 20-APR-1992; 92US-0872644.
 PR 19-APR-1991; 91US-0688356.
 PR 29-AUG-1994; 94US-0297494.
 XX (UNIV) UNIV WASHINGTON.
 XX Beavo JA, Bentley JK, Charbonneau H, Sonnenburg WK;
 WPI: 1998-398038/34.
 DR N-PSDB; FAV36148.
 XX New calmodulin and calcium stimulated cyclic nucleotide
 PT phosphodiesterase - used e.g. to identify selective modulators,
 PT potentially useful as e.g. cardiotoxic, antidepressant,
 PT antihypertensive agents
 XX Claim 3: Columns 57-60; 69pp; English.
 XX The present sequence represents 63 kDa calcium ion/calmodulin stimulated
 CC cyclic nucleotide phosphodiesterase (Cam-PDE) polypeptide, isolated from
 CC bovine brain. Cam-PDEs are characterised by their responsiveness
 CC to intracellular calcium, which leads to a decreased intracellular
 CC concentration of cAMP and/or cGMP. Cam-PDEs, and their fragments or
 CC synthetic peptides, are used in therapy, prognosis and diagnosis. They
 CC are also used to generate specific antibodies useful as immunoassay
 CC reagents for detecting the protein or for affinity purification and for
 CC identifying specific modulators of Cam-PDE activity. Cam-PDEs are
 CC implicated in signalling involving extracellular hormones and
 CC neurotransmitters, so selective inhibitors are potentially useful as
 CC cardiotoxic, antidepressant, antihypertensive and antithrombotic agents.

XX Sequence 534 AA;

Query Match 92.8%; Score 2484.5; DB 19; Length 534;
 Best Local Similarity 96.0%; Pred. No. 1.2e-226;
 Matches 478; Conservative 10; Mismatches 9; Indels 1; Gaps 1;

QY 19 LRYMVKQLENGEINIEELKKNLEYTASLLEAVYIDETROILDELOELRSDAVPSEVR 78
 DB 38 LRYMVKQLENGEINIEELKKNLEYTASLLEAVYIDETROILDELOELRSDAVPSEVR 97
 QY 79 DWLASTFTQOARAKGRRAEKPFRSIVHAVQAGIFVERMFRRTYTSVGPSTAVLNCL 138
 DB 98 DWLASTFTQOARAKGRRAEKPFRSIVHAVQAGIFVERMFRRTYTSVGPSTAVLNCL 156
 QY 139 KNLDLWCFDVSFSLNOADDDHALRTIVFELLTRNLISRPKIPVFLMSFLDALETGYGY 198
 DB 157 KNVDLWCFDVSFSLNOADDDHALRTIVFELLTRNLISRPKIPVFLMSFLDALETGYGY 216
 QY 199 KNPYHNOIHAADVTQVHCFLRTGVMVHCLSEIELLAIIFAAAIHDYEHGTGTTNSPHIOT 258
 DB 217 KNPYHNOIHAADVTQVHCFLRTGVMVHCLSEIELLAIIFAAAIHDYEHGTGTTNSPHIOT 276
 QY 259 KSECAIYNDRSVLENHHISSVFRMLQDDMMNIFNLTKDEFVELRALVIEMVLATDMSC 318
 DB 277 KSECAIYNDRSVLENHHISSVFRMLQDDMMNIFNLTKDEFVELRALVIEMVLATDMSC 336
 QY 319 HFQOVKMTALQOQLERIDPKALSLLLHAADISHPTKQWLIVHSRWTKALMEEFPRQGDK 378
 DB 337 HFQOVKMTALQOQLERIDPKALSLLLHAADISHPTKQWLIVHSRWTKALMEEFPRQGDK 396
 QY 379 EAEGLGFPSPCLDRTSTLVAQSQIGFIDFIVEPTFSLTDVAEKSVQPLADEDSKSNOP 438
 DB 397 EAEGLGFPSPCLDRTSTLVAQSQIGFIDFIVEPTFSLTDVAEKSVQPLADEDSKSNOP 456
 QY 439 SFQWRQPSLDVEGDPNPVSPRSTWTKYIQENKQKWKERAAAGITNOMSIDELSPCEE 498

Db 457 SFQWRQPSLDVEGDPNPVVSFRSTWTKYIOENKQKWKRAASGITNOMSIDELSPCEE 516
 QY 499 EAPSPAEDHNQNGNLD 516
 Db 517 EAPSPAEDHNQNGNLD 534

RESULT 9

AAAY80977
 ID AAY80977 standard; Protein: 534 AA.

AC AAY80977;

DT 05-JUN-2000 (first entry)

DE Bovine brain 63 kD CaM-PDE clone p12.3a protein, SEQ ID NO:27.

XX Phosphodiesterase; calcium; calmodulin; cyclic guanine monophosphate;
 KW cGMP; cyclic nucleotide; messenger; signal transduction; regulation;
 KW inhibitor; cardiotonic; antidepressant; antihypertensive;
 KW antithrombotic.

XX Bos taurus.

XX US6015677-A.

XX 18-JAN-2000.

XX 25-AUG-1998; 98US-0139491.

XX 20-APR-1992; 92US-0872644.

XX 29-AUG-1994; 94US-0297494.

XX 31-MAY-1995; 95US-0455525.

XX 19-APR-1991; 91US-0688356.

XX (UNIW) UNIV WASHINGTON.

XX Charbonneau H, Sonnenburg WK, Bentley KJ, Beavo JA;

XX WPI: 2000-181142/16.

XX N-PSDB; AA290372.

XX Assay for inhibitors of cyclic guanine monophosphate-stimulated

XX nucleotide phosphodiesterase, potentially useful as cardiotonic agents,

XX from their ability to alter a heat-shock phenotype

XX Example III; Column 57-60; 69pp; English.

XX The invention relates to purified and isolated nucleotide sequences
 CC encoding mammalian Ca2+/calmodulin-stimulated phosphodiesterases
 CC (CaM-PDEs) and cyclic guanine monophosphate (cGMP)-stimulated
 CC phosphodiesterases (cGS-PDEs). In particular the invention relates to an
 CC assay for identifying chemicals that modify the enzymatic activity of
 CC a mammalian cGS-PDE. The PDEs catalyse the hydrolysis of cyclic
 CC nucleotides to their corresponding 5'-nucleoside monophosphates. In this
 CC way they control the cellular concentration of cyclic nucleotides,
 CC thereby regulating the flow of information from extracellular hormones,
 CC neurotransmitters or other signals that use cyclic nucleotides as
 CC messengers. The PDEs in turn are regulated by transmembrane signals
 CC or second messenger ligands such as Ca2+ or cGMP. Inhibitors of these
 CC enzymes are potentially useful as cardiotonics, antidepressants,
 CC antihypertensives or antithrombotics. The method of the invention can
 CC identify specific inhibitors of particular isoforms of cGS-PDEs.
 CC Sequences AAY80968, AAY80972, AAY80975, AAY80984-Y80986, and
 CC AAY80988-Y80990 represent isoforms of CaM-PDEs and cGS-PDEs from bovines
 CC and humans.

XX Sequence 534 AA;

XX Query Match

XX Best Local Similarity 92.8%; Score 2484.5; DB 21; Length 534;

XX Matches 478; Conservative 10; Mismatches 9; Indels 1; Gaps 1;

QY 19 LRYMVKQLENGEINTEELKKNLEYTASLEAVYIDETROIILDTDEQLRSDAVPSEVR 78
 Db 38 LRYMVKQLENGEINTEELKKNLEYTASLEAVYIDETROIILDTDEQLRSDAVPSEVR 97
 QY 79 DWLASTFTQARAKGRRAEKPFRSIVHAQVAGIFVERMFRRTVTSVGPTYSTAVLNCL 138
 Db 98 DWLASTFTQOTRAKG-PSEKPKFRSIVHAQVAGIFVERMFRRTVTSVGPTYSTAVLNCL 156
 QY 139 KNLDLWCFDVSLSNQAADHALRTIVFELLFRHNLSIRFKIPTVFLMSFLDALETGYGKY 198
 Db 157 KNVDLWCFDVSLSNRAADHALRTIVFELLFRHNLSIRFKIPTVFLMTFLDALETGYGKY 216
 QY 199 KNPYHNOIHAADVOTVHCFLRLTGMVHCLSEIELLAIIFAAAIHDYEHGTGTTNSFHQT 258
 Db 217 KNPYHNOIHAADVOTVHCFLRLTGMVHCLSEIELLAIIFAAAIHDYEHGTGTTNSFHQT 276
 QY 259 KSECAIVNDRSVLENHHISSVFRMLQDDNMNIFNLTKDFEVLRLVIEMLVATDMSC 318
 Db 277 KSECAILYNDRSVLENHHISSVFRMWQDDNMNIFNLTKDFEVLRLVIEMLVATDMSC 336
 QY 319 HFQVQVTKMTALQQLERIDKPKALSLLHAADISHPTKQWLVHSRWTALMEEFFRQGDK 378
 Db 337 HFQVQVTKMTALQQLERIDKPKALSLLHAADISHPTKQWLVHSRWTALMEEFFRQGDK 396
 QY 379 EAEGLPFSPLCDRTSTLVAOSQIGFIDFIVEPTESVLTDAEKSQVPLADEDSKSNQP 438
 Db 397 EAEGLPFSPLCDRTSTLVAOSQIGFIDFIVEPTESVLTDAEKSQVQTDGDDSKSNQP 456
 QY 439 SFQWRQPSLDVEGDPNPVVSFRSTWTKYIOENKQKWKRAASGITNOMSIDELSPCEE 498
 Db 457 SFQWRQPSLDVEGDPNPVVSFRSTWTKYIOENKQKWKRAASGITNOMSIDELSPCEE 516
 QY 499 EAPSPAEDHNQNGNLD 516
 Db 517 EAPSPAEDHNQNGNLD 534

RESULT 10

ABUS8716
 ID ABUS8716 standard; Protein: 534 AA.

XX AC ABUS8716;

XX DT 15-APR-2003 (first entry)

XX DE Bovine brain 63kDa CaM-PDE variant #1.

XX KW Cow; Ca2+/calmodulin stimulated phosphodiesterase; enzyme;
 KW Cam-PDE; 59KDa CaM-PDE; 61kDa CaM-PDE; 63kDa CaM-PDE; cGS-PDE;
 KW cyclic-GMP-stimulated phosphodiesterase; cardiotonic agent;
 KW antidepressant; anti-hypertensive; anti-thrombotic.

XX OS Bos taurus.

XX PN US2002151024-A1.

XX PD 17-OCT-2002.

XX PF 18-JUN-2001; 2001US-0883825.

XX PR 20-APR-1992; 92US-0872644.

XX PR 31-MAY-1995; 95US-0455526.

XX PR 28-JUL-1998; 98US-0123783.

XX PR 19-APR-1991; 91US-0688356.

XX PA (UNIW) UNIV WASHINGTON.

XX PI Beavo JA, Bentley JK, Charbonneau H, Sonnenburg WK;

XX WPI; 2003-198291/19.

XX DR N-PSDB; ABX78849.

PT New purified and isolated DNA sequence encoding a mammalian
 PT calcium/calmodulin- or cyclic GMP-stimulated cyclic nucleotide
 PT phosphodiesterase polypeptide, useful for therapeutic, diagnostic and
 XX prognostic applications -

XX Example 3; Page 32-33; 71pp; English.

XX The invention relates to purified and isolated polynucleotide sequence
 CC encoding a mammalian Ca²⁺/calmodulin- or cyclic GMP-stimulated cyclic
 CC nucleotide phosphodiesterase polypeptide (CaMP-PDE and CGS-PDE).
 CC Also included are a DNA vector comprising the novel DNA sequence, a host
 CC cell transformed with the polynucleotide sequence, a polypeptide product
 CC of the expression in the transformed host cell, an antibody specifically
 CC immunoreactive with the polypeptide and assay methods for identifying a
 CC chemical agent which modifies the enzymatic activity of a mammalian
 CC CaMP-PDE or CGS-PDE. Disclosed are the cDNA and protein sequences
 CC of bovine 59kDa CaM-PDE, 61kDa CaM-PDE, 63kDa CaM-PDE, CGS-PDE and
 CC human 61kDa CaM-PDE and CGS-PDE. The DNA sequence is useful for producing
 CC a polypeptide having the enzymatic activity of a mammalian CaM-PDE or
 CC CGS-PDE which is used in the therapeutic, diagnostic and prognostic
 CC applications and in the preparation of antibodies. Isolated chemical
 CC agents which are inhibitors of PDEs may have anti-depressant, anti-
 CC hypertensive or anti-thrombotic activities or may be cardiotoxic agents.
 CC The present sequence is a Bovine CaM-PDE or CGS-PDE (or fragment) of the
 XX invention.

XX Sequence 534 AA;

Query Match 92.6%; Score 2484.5; DB 24; Length 534;
 Best Local Similarity 96.6%; Pred. No. 1.2e-226;
 Matches 478; Conservative 10; Mismatches 9; Indels 1; Gaps 1;
 QY 19 LRYWVKQLENGEINIEELKKNLEYTASILEAVYIDETROILOLDELQELSDAVPSEVR 78
 Db 38 LRYWVKQLENGEINIEELKKNLEYTASILEAVYIDETROILOLDELQELSDAVPSEVR 97
 QY 79 DWLASTFTQOARAKGRRAEKPFRSIVHVAQAGIFVERMFRRTYTSVGTPTYSTAVLNCL 138
 Db 98 DWLASTFTQOARAKGRRAEKPFRSIVHVAQAGIFVERMFRRTYTSVGTPTYSTAVLNCL 156
 QY 139 KNLDLWCFDVFSLNQADHDHALRTIVFELLTRHNLISRFKIPTVFLMSFLDALETGYGKY 198
 Db 157 KNLDLWCFDVFSLNQADHDHALRTIVFELLTRHNLISRFKIPTVFLMSFLDALETGYGKY 216
 QY 199 KNPYHNQIHAADVDTQVHCFLLRTGMVHCLSEIELLAIIFAAAIHDYEHGTGTTNSFHIQT 258
 Db 217 KNPYHNQIHAADVDTQVHCFLLRTGMVHCLSEIELLAIIFAAAIHDYEHGTGTTNSFHIQT 276
 QY 259 KSCAIVYNDRSVLENHHISSVFRMQDDMMNIFNLTKDEFVELRALVEMVLATDMSC 318
 Db 277 KSCAIVYNDRSVLENHHISSVFRMQDDMMNIFNLTKDEFVELRALVEMVLATDMSC 336
 QY 319 HFQOVKMTALQQLERIDKPKALSLLHAADISHPTKOWLVHSRWTKALMEEFTRQDK 378
 Db 337 HFQOVKMTALQQLERIDKPKALSLLHAADISHPTKOWLVHSRWTKALMEEFTRQDK 396
 QY 379 EAELGLPFPCLDRTSTLVAQSQIGFIDFIVEPTFSVLTDVAEKSVQPTGDDSKKNOP 438
 Db 397 EAELGLPFPCLDRTSTLVAQSQIGFIDFIVEPTFSVLTDVAEKSVQPTGDDSKKNOP 456
 QY 439 SFQWRQPSLDVEGDPNDVFSRSTWVKRIQENKQKWKERASGTTNOMSIDELSPCEE 498
 Db 457 SFQWRQPSLDVEGDPNDVFSRSTWVKRIQENKQKWKERASGTTNOMSIDELSPCEE 516
 QY 499 EAPPSAEDEHNGNGLD 516
 Db 517 EAPPSAEDEHNGNGLD 534

RESULT 11

AAR28404
 ID AAR28404 standard; Protein; 534 AA.
 XX

AC AAR28404;
 XX 25-MAR-2003 (updated)
 DT 19-MAR-1993 (first entry)
 XX
 DE 63 kD CaM PDE from clone p12.3a from bovine brain.
 XX
 KW Calcium/calmodulin; stimulated; cyclic; nucleotide;
 KW phosphodiesterase.
 XX
 OS Bos taurus.
 XX
 FH Key Location/Qualifiers
 FT Region 44..57
 FT /note= "homology with aligned peptides from 63kD CaM PDE"
 FT Region 277..292
 FT /note= "homology with aligned peptides from 63kD CaM PDE"
 XX
 PN W09218541-A1.
 XX
 PD 29-OCT-1992.
 XX
 PF 20-APR-1992; 92WO-US03222.
 XX
 PR 19-APR-1991; 91US-0688356.
 XX
 PA (UNIW) UNIV WASHINGTON.
 XX
 PI Beavo JA, Bentley JK, Charbonneau H, Sonnenburg WK;
 XX WPI; 1992-382051/46.
 DR N-PSDB; AAQ30175.
 XX
 PT New DNA encoding mammalian cyclic nucleotide phospho-di:esterase
 PT - and derived vectors and host cells, useful for screening cpds.
 PT for inhibitory or activating activity
 XX
 PS Example 3; Page 76; 133pp; English.
 XX
 CC Oligonucleotide 63-1s, a fully redundant 23-mer was used to screen a
 CC total bovine brain cDNA library in lambda ZAP II. A total of 21
 CC putative positives were picked and rescreened with the probe from
 CC plasmid p11.5b. One positive was obtd. designated p12.3a, which
 CC codes for a protein sequence with most of the aligned peptides
 CC isolated from bovine 63 kD CaM PDE.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 534 AA;

Query Match 92.6%; Score 2478.5; DB 13; Length 534;
 Best Local Similarity 95.6%; Pred. No. 4.3e-226;
 Matches 476; Conservative 12; Mismatches 9; Indels 1; Gaps 1;
 QY 19 LRYWVKQLENGEINIEELKKNLEYTASILEAVYIDETROILOLDELQELSDAVPSEVR 78
 Db 38 LRYWVKQLENGEINIEELKKNLEYTASILEAVYIDETROILOLDELQELSDAVPSEVR 97
 QY 79 DWLASTFTQOARAKGRRAEKPFRSIVHVAQAGIFVERMFRRTYTSVGTPTYSTAVLNCL 138
 Db 98 DWLASTFTQOARAKGRRAEKPFRSIVHVAQAGIFVERMFRRTYTSVGTPTYSTAVLNCL 156
 QY 139 KNLDLWCFDVFSLNQADHDHALRTIVFELLTRHNLISRFKIPTVFLMSFLDALETGYGKY 198
 Db 157 KNLDLWCFDVFSLNQADHDHALRTIVFELLTRHNLISRFKIPTVFLMSFLDALETGYGKY 216
 QY 199 KNPYHNQIHAADVDTQVHCFLLRTGMVHCLSEIELLAIIFAAAIHDYEHGTGTTNSFHIQT 258
 Db 217 KNPYHNQIHAADVDTQVHCFLLRTGMVHCLSEIELLAIIFAAAIHDYEHGTGTTNSFHIQT 276
 QY 255 KSCAIVYNDRSVLENHHISSVFRMQDDMMNIFNLTKDEFVELRALVEMVLATDMSC 318
 Db 277 KSCAIVYNDRSVLENHHISSVFRMQDDMMNIFNLTKDEFVELRALVEMVLATDMSC 336

QY 319 HFQVQVTKMTALQQLERIDKPKALSLLHAADISHPTKOWLVHRSWTKALMEEFPROGDK 378
 Db 337 HFQVQVSMKMTALQQLERIDKSKALSLLHAADISHPTKOWSVHRSWTKALMQEFPROGDK 396
 QY 379 EAEGLPSPCLDRSTSLVAQSQIGFIDFIVEPTSVLTDVAEKSVQPLADEDSKSNOP 438
 Db 397 EAEGLPSPCLDRSTSLVAQSQIGFIDFIVEPTSVLTDVAEKSVQPTGDDDSKSNOP 456
 QY 439 SFQWRQPSLDVEGDPNDVVSFRSTWTKRIQENKQKERAASGITNOMSIDELSPCEE 498
 Db 457 SFQWRQPSLDVEGDPNDVVSFRSTWTKYIQENKQKERAASGITNOMSIDELSPCEE 516
 QY 499 EAPSPAPDEHNQNGNLD 516
 Db 517 EAPSPAPDEHNQNGNLD 534

RESULT 12

.ID AAR69715 standard; Protein; 514 AA.

AC AAR69715;

DT 25-MAR-2003 (updated)

DT 11-OCT-1995 (first entry)

DE Cyclic-GMP stimulated nucleotide PDE clone p59KCAMPDE-2.

KW Cyclic-GMP stimulated nucleotide phospho-diesterase;

KW bovine lung; hormones; neurotransmitters; transmission regulation;

KW antibodies; enzyme purification; clone p59CAMPDE-2.

XX Bos taurus.

XX US5389527-A.

XX 14-FEB-1995.

XX 20-APR-1992; 92US-0872644.

XX 19-APR-1991; 91US-0688356.

XX 20-APR-1992; 92US-0872644.

PA (UNIW) UNIV WASHINGTON.

PI Beavo JA, Charbonneau H, Sonnenburg WK;

XX WPI; 1995-090205/12.

DR N-PSDB; AAQ83964.

XX New nucleic acid encoding cyclic-GMP stimulated nucleotide

PT phospho-diesterase - and related vectors and transformed cells,

PT useful for screening cpds. for phospho-di:esterase modulating

PT activity

XX Example 2; Columns 43-48; 69pp; English.

XX AAQ83964 encodes AAR69715 bovine lung cyclic-GMP stimulated nucleotide

CC phospho-diesterase (Cam PDE) clone p59KCAMPDE-2. Eukaryotic cells

CC that express Cam PDE can be used to screen cpds. for the ability to

CC modulate Cam PDE activity. Cam PDEs are involved in regulating

CC the transmission of information from hormones, neurotransmitters

CC or other systems that use cyclic nucleotides as messengers.

CC Antibodies raised against Cam PDE can be used for enzyme purific.,

CC or determination.

CC (Updated on 25-MAR-2003 to correct PF field.)

XX Sequence 514 AA;

Query Match

Best Local Similarity 61.2%; Score 1636.5; DB 16; Length 514;

Matches 309; Conservative 94; Mismatches 96; Indels 9; Gaps 1;

QY 1 MANPVQVSHLQGPILRLRYVMVKOLENGEINIEELKKNLEYTASLLAEVYIDETRLQILD 60
 Db 1 MDDHVTIRKHLQRFIFRLCLVKLEKGDVNVIDLKKNIEYAAVSAVLEAVYIDETRLULD 60
 QY 61 TEDELOELRSADVSEVRDNLASTTQOARAKRAEAEKPKRPSIVHAVQAGIFVERMFR 120
 Db 61 TDDELSDIQSDSPVSEVRDNLASTTFRKMGMMKKSEKPKRPSIVHVQAGIFVERMYR 120
 QY 121 RYTSVSGPTYSTAVLNCNLKNDLWCFDVSFLNOAADHALRTIVFELTRHNLISRFKIP 180
 Db 121 KSYHVMGLAYPAVIVITLKDVKNSFDVFNALNEASGEHSLKPMIYELFTRYDLINRFKIP 180
 QY 181 TVFLMSFLDALGETGYKYNPNYHNIHAADVTQTVHCFLLRTGMVHCLSEIELLAIIFAA 240
 Db 181 VSLCIAFAEALEVGYSKYKNPYHNLHAADVTQTVHYIMLHTGIMHMLTELEILAMVFAA 240
 QY 241 AIHDEHTGTNSFIQTKECAIYVNDRSVLENHIISSVFLMQDDENINILTKDEF 300
 Db 241 AIHDEHTGTNNFIQTRSDVAILYNDRSVLENHVSAAAYRLMQDEENMVLINLSKDDM 300
 QY 301 VELRALVTEMVLATDMSCHFOOVTKMTALQQLERIDKPKALSLLHAADISHPTKOWLV 360
 Db 301 RDLRLNVLEMVLSTDMSGHFOQIKNIRNSLQOPEGLDKAKTMSLILHAADISHPAKSWKL 360
 QY 361 HSRWTKALMEEFPROGDKAEALGLPSPCLDRSTSLVAQSQIGFIDFIVEPTSVLTDVA 420
 Db 361 HHRWTMALMEEFPROGDKAEALGLPSPCLDRKSTWVAQSQIGFIDFIVEPTFSLTDTST 420
 QY 421 EKSVOPLADEDSKSNQPSFQWRQPSLDVEGCD-----PNDVVSFRSTWTKRIQE 471
 Db 421 EKIIITFEEDSKTKTPSYGASRRGNMKGTNDGTYSYDYSVLASVDLAKSFKNLSLVDIIQO 480
 QY 472 NKQWKERAASGITNOMSIDELSPCEE 499
 Db 481 NKERWELAAQGEPPDHKNSDLVNAEEK 508

RESULT 13

AAW18037

ID AAW18037 standard; protein; 514 AA.

XX AC AAW18037;

XX 25-MAR-2003 (updated)

DT 31-JUL-1997 (first entry)

DE Bovine lung 59 kDa Ca2+/calmodulin stimulated phosphodiesterase.

XX Ca2+/calmodulin stimulated cyclic nucleotide phosphodiesterase enzyme;

KW calcium ion; Cam-PDE; antibody; cow.

OS Bos taurus.

XX US5602019-A.

XX 11-FEB-1997.

XX 29-AUG-1994; 94US-0297510.

XX 20-APR-1992; 92US-0872644.

PR 19-APR-1991; 91US-0688356.

PR 29-AUG-1994; 94US-0297510.

XX (UNIW) UNIV WASHINGTON.

XX Sonnenburg WK, Charbonneau H, Bentley JK, Beavo JA;

PI WPI; 1997-131799/12.

DR N-PSDB; AAT67199.

XX DNA encoding bovine and human phosphodiesterase enzymes - stimulated
 PT by calcium/calmodulin, useful for recombinant prodn. of the enzymes
 XX

```

PS Example 2; Column 47-50; 69pp; English.
XX
XX The present sequence represents 59 kDa Ca2+/calmodulin-stimulated
CC cyclic nucleotide phosphodiesterase (Cam-PDE) enzyme derived from
CC bovine lung. The DNA sequences are used for the production of the
CC recombinant enzymes, which in turn may be used for antibody
CC production and to screen for compounds that modulate phosphodiesterase
CC activity.
CC (Updated on 25-MAR-2003 to correct PF field.)
CC (Updated on 25-MAR-2003 to correct PI field.)
XX
XX Sequence 514 AA;

Query Match 61.2%; Score 1636.5; DB 18; Length 514;
Best Local Similarity 60.8%; Pred. No. 3.3e-146;
Matches 309; Conservative 94; Mismatches 96; Indels 9; Gaps 1;

Qy 1 MANPVPVQRSHLQGPILRLRYMVKOLENGEINIEELKKNLEYTASLLEAVYIDETRIQLD 60
Db | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
1 MDDHVTIRKKLQRPFRRLRCLVKOLEKGDVNVIDLKKNIEYAASVLEAVYIDETRRLLD 60

Qy 61 TEDELQELRSADVSEVRDMLASTFTQOARAKGRAEKPFRSIVHVAQAGIFVERMFR 120
Db | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
61 TDDELSDIQSDSVSEVRDMLASTFTFRKMGMMKKSEKPRFSIVHVYQAGIFVERMYR 120

Qy 121 RTYTSVGPYTSYAVLNCNLKLDLWCFDVSFNQAADHALRTIVPELLTRHNLISRFKIP 180
Db | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
121 KSYHMVGLAYPEAVITVTLKDVKWSDFVFNQAADHALRTIVPELLTRHNLISRFKIP 180

Qy 181 TVFLMSFLDALETGYGKYKNPNYHNOIHAADVTQTVHCFLLRTGMVHCLSEIELLAF 240
Db | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
181 VSLIAFAEALEVGYSKYKNPNYHNLJHAADVTQTVHYIMLHTGIMHLTELELAWFAA 240

Qy 241 AIHDEYHTGTTNSFHIOKSECAIVYNDRSVLENHHISSVFLMODDNNIINTKDEF 300
Db | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
241 AIHDEYHTGTTNNFHIOKSECAIVYNDRSVLENHHISSVFLMODDNNIINTKDEF 300

Qy 301 VELRALVTEMVLATDMSCHFOOVKMTALQOLERIDPKALSLLLHAAIDSHPTKQW 360
Db | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
301 RDLRLNVLTEMVLSTMSGSHFQOIKNIRNSLQOPEGLDKRAKTMSLLLHAAIDSHPTKQW 360

Qy 361 HSRWTKALMEEFFRQGDKEAELGLPFLPCDRTSTFLVAQSQIGFDIVPEPTFSLTDT 420
Db | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
361 HHRWTMALMEEFFRQGDKEAELGLPFLPCDRTSTFLVAQSQIGFDIVPEPTFSLTDT 420

RESULT 14
AAW11240
XX
XX AAW11240 standard; Protein; 514 AA.
AC
XX
XX AAW11240;
AC
XX
XX 25-MAR-2003 (updated)
DT
XX
XX 17-MAR-1997 (first entry)
DT
XX
XX Calcium/calmodulin dependent phosphodiesterase.
DE
XX
XX Cyclic GMP stimulated phosphodiesterase; cGS-PDE; bovine; brain; CAMP;
KW adrenal gland; transmembrane signal; extracellular hormone; antibody;
KW neurotransmitter; cGMP; calcium/calmodulin dependent phosphodiesterase;
KW Cam-PDE.
XX
XX Bos taurus.
XX
XX US5580771-A.
PN

```

This sequence represents the calcium/calmodulin dependent phosphodiesterase (Cam-PDE) clone p59KAMPDE-2 isolated from bovine lung. The cyclic nucleotide phosphodiesterases (PDEs) catalyse the hydrolysis of 3', 5' cyclic nucleotides, such as cAMP and cGMP, to their corresponding 5'-nucleotide monophosphates. The PDEs are therefore important in the control of the cellular concentration of cyclic nucleotides. The PDEs are, in turn, regulated by transmembrane signals or second messenger ligands such as calcium ion or cGMP. The PDEs therefore have a central role in regulating the flow of information from extracellular hormones, neurotransmitters, or other signals that use the cyclic nucleotides as messengers. PDEs are present in most of the cells and tissues of eukaryotic organisms, but only trace amounts of Cam-PDEs are responsive to intracellular calcium, which leads to decreased intracellular concentration of cAMP, and/or cGMP. The DNA encoding this sequence can be used for the production of recombinant Cam-PDE, which may have therapeutic and diagnostic uses. This sequence may also be useful for diagnostic antibody production. (Updated on 25-MAR-2003 to correct PF field.)

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OM protein - protein search, using sw model

Run on: August 11, 2003, 01:06:37 ; Search time 43 Seconds
(without alignments)
507.730 Million cell updates/sec

Title: US-09-663-481-1
Perfect score: 2676
Sequence: 1 MANPVPVQRSHLQGFILRL.....EEAPPSAEDEHNGNGLD 516

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2.6/ptodata/1/1aa/5A_COMB.pep.*
2: /cgn2.6/ptodata/1/1aa/5B_COMB.pep.*
3: /cgn2.6/ptodata/1/1aa/6A_COMB.pep.*
4: /cgn2.6/ptodata/1/1aa/6B_COMB.pep.*
5: /cgn2.6/ptodata/1/1aa/PCTUS_COMB.pep.*
6: /cgn2.6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2592	96.5	536	2	US-08-940-332-2
2	2484.5	92.8	534	1	US-07-872-644-27
3	2484.5	92.8	534	1	US-08-297-494-27
4	2484.5	92.8	534	1	US-08-297-510-27
5	2484.5	92.8	534	1	US-08-479-532-27
6	2484.5	92.8	534	1	US-08-455-526-27
7	2484.5	92.8	534	1	US-08-455-525-27
8	2484.5	92.8	534	3	US-09-139-491-27
9	2484.5	92.8	534	5	PCT-US92-03222-27
10	1636.5	61.2	514	1	US-07-872-644-17
11	1636.5	61.2	514	1	US-08-297-494-17
12	1636.5	61.2	514	1	US-08-297-510-17
13	1636.5	61.2	514	1	US-08-479-532-17
14	1636.5	61.2	514	1	US-08-455-526-17
15	1636.5	61.2	514	1	US-08-455-525-17
16	1636.5	61.2	514	3	US-09-139-491-17
17	1636.5	61.2	514	5	PCT-US92-03222-17
18	1593	59.5	534	1	US-07-872-644-51
19	1593	59.5	534	1	US-08-297-494-51
20	1593	59.5	534	1	US-08-297-510-51
21	1593	59.5	534	1	US-08-479-532-51
22	1593	59.5	534	1	US-08-455-526-51
23	1593	59.5	534	1	US-08-455-525-51
24	1593	59.5	534	3	US-09-139-491-51
25	1593	59.5	534	5	PCT-US92-03222-51
26	1591.5	59.5	530	1	US-07-872-644-6
27	1591.5	59.5	530	1	US-08-297-494-6

28	1591.5	59.5	530	1	US-08-297-510-6	Sequence 6, Appl1
29	1591.5	59.5	530	1	US-08-479-532-6	Sequence 6, Appl1
30	1591.5	59.5	530	1	US-08-455-526-6	Sequence 6, Appl1
31	1591.5	59.5	530	1	US-08-455-525-6	Sequence 6, Appl1
32	1591.5	59.5	530	3	US-09-139-491-6	Sequence 6, Appl1
33	1591.5	59.5	530	5	PCT-US92-03222-6	Sequence 6, Appl1
34	1568.5	58.6	535	1	US-07-872-644-49	Sequence 49, Appl
35	1568.5	58.6	535	1	US-08-297-494-49	Sequence 49, Appl
36	1568.5	58.6	535	1	US-08-297-510-49	Sequence 49, Appl
37	1568.5	58.6	535	1	US-08-479-532-49	Sequence 49, Appl
38	1568.5	58.6	535	1	US-08-455-526-49	Sequence 49, Appl
39	1568.5	58.6	535	1	US-08-455-525-49	Sequence 49, Appl
40	1568.5	58.6	535	3	US-09-139-491-49	Sequence 49, Appl
41	1568.5	58.6	535	5	PCT-US92-03222-49	Sequence 49, Appl
42	1206	45.1	564	1	US-07-872-644-53	Sequence 53, Appl
43	1206	45.1	564	1	US-08-297-494-53	Sequence 53, Appl
44	1206	45.1	564	1	US-08-297-510-53	Sequence 53, Appl
45	1206	45.1	564	1	US-08-479-532-53	Sequence 53, Appl

ALIGNMENTS

RESULT 1
US-08-940-332-2
; Sequence 2, Application US/08940332
; Patent No 5885834
; GENERAL INFORMATION:
; APPLICANT: Epstein, Paul M.
; TITLE OF INVENTION: SYNTHESIS OF ANTISENSE
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE OF PHOSPHODIESTERASE AND
; TITLE OF INVENTION: INDUCEMENT OF APOPTOSIS IN HUMAN LYMPHOBLASTOID CELLS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ALIX, YALE & RISTAS, LLP
; STREET: 750 MAIN STREET
; CITY: HARTFORD
; STATE: CT
; COUNTRY: USA
; ZIP: 06103-2721
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/940,332
; FILING DATE: 30-SEP-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/027,207
; FILING DATE: 30-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Alix, James E.
; REGISTRATION NUMBER: 20,736
; REFERENCE/DOCKET NUMBER: UCON/137/US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (860)527-9211
; TELEFAX: (860)527-5029
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 536 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-940-332-2

Query Match 96.5%; Score 2582; DB 2; Length 536;
Best Local Similarity 100.0%; Pred. No. 1.3e-244;
Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 19 LRYMVKQLNGEINTEELKKNLEYTASLLEAVYIDETROIILDTDELQELRSDAVPSEVR 78
DB 39 LRYMVKQLNGEINTEELKKNLEYTASLLEAVYIDETROIILDTDELQELRSDAVPSEVR 98

QY 79 DWLASTTQOARAKGRRAEKPFRSIVHVAQAGIFVERMFRRTYTSVGPTYSTAVLNCL 138
DB 99 DWLASTTQOARAKGRRAEKPFRSIVHVAQAGIFVERMFRRTYTSVGPTYSTAVLNCL 158
QY 139 KNLDLWCDFVSLNQADDDHALRTIVFELLTRHNLISREKIPITVFLMSFLDALETGYGKY 198
DB 159 KNLDLWCDFVSLNQADDDHALRTIVFELLTRHNLISREKIPITVFLMSFLDALETGYGKY 218
QY 199 KNPYHNOIHAADVTQTVHCFLLRTGMVHCLSEIELLAIIFAAAHHDYEHTGTTNSPHIQT 258
DB 219 KNPYHNOIHAADVTQTVHCFLLRTGMVHCLSEIELLAIIFAAAHHDYEHTGTTNSPHIQT 278
QY 259 KSECAIYVNDRSVLENHHSVFLMDDDMNIFINLTDEFFELRALVTEMVLATDMSC 318
DB 279 KSECAIYVNDRSVLENHHSVFLMDDDMNIFINLTDEFFELRALVTEMVLATDMSC 338
QY 319 HFQOVKMTALQOQLERIDPKKALSLLLHAADISHPTKQWLHVSRTWKALMEEFFRQGD 378
DB 339 HFQOVKMTALQOQLERIDPKKALSLLLHAADISHPTKQWLHVSRTWKALMEEFFRQGD 398
QY 379 EAEGLPSPCLCDRTSTLVAQSQIGFDIFVEPTFSVLTDAEKSVOPLADEDSKSNQP 438
DB 399 EAEGLPSPCLCDRTSTLVAQSQIGFDIFVEPTFSVLTDAEKSVOPLADEDSKSNQP 458
QY 439 SFOWRQPSLDVEGDPNDPVVSRSTWVKRIQENKQWKERRAASGITNQMIDELSPCEE 498
DB 459 SFOWRQPSLDVEGDPNDPVVSRSTWVKRIQENKQWKERRAASGITNQMIDELSPCEE 518
QY 499 EAPPSPAEDEHNGNGLD 516
DB 519 EAPPSPAEDEHNGNGLD 536

RESULT 2

US-07-872-644-27 Application US/07872644
Sequence 27, Patent No. 5389527

GENERAL INFORMATION:

APPLICANT: Beavo, Joseph A.
APPLICANT: Bentley, Kelley
APPLICANT: Charbonneau, Harry
APPLICANT: Sonnenburg, William K.
TITLE OF INVENTION: DNA Encoding Mammalian
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/872,644
FILING DATE: 19920420
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/688,356
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5389527 and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30822
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750

TELEFAX: (312) 984-9740

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:

LENGTH: 534 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: protein

US-07-872-644-27

Query Match 92.8%; Score 2484.5; DB 1; Length 534;
Best Local Similarity 96.0%; Pred No. 4.9e-235;
Matches 476; Conservative 9; Mismatches 9; Indels 1; Gaps 1;

QY 19 LRYWVQLENGEINIEELKNLEYTASLLAEVYIDETROQLDTEDELEQLRSDAVPSEVR 78
DB 38 LRYWVQLENGEINIEELKNLEYTASLLAEVYIDETROQLDTEDELEQLRSDAVPSEVR 97
QY 79 DWLASTTQOARAKGRRAEKPFRSIVHVAQAGIFVERMFRRTYTSVGPTYSTAVLNCL 138
DB 98 DWLASTTQOARAKGRRAEKPFRSIVHVAQAGIFVERMFRRTYTSVGPTYSTAVLNCL 156
QY 139 KNLDLWCDFVSLNQADDDHALRTIVFELLTRHNLISREKIPITVFLMSFLDALETGYGKY 198
DB 157 KNLDLWCDFVSLNQADDDHALRTIVFELLTRHNLISREKIPITVFLMSFLDALETGYGKY 216
QY 199 KNPYHNOIHAADVTQTVHCFLLRTGMVHCLSEIELLAIIFAAAHHDYEHTGTTNSPHIQT 258
DB 217 KNPYHNOIHAADVTQTVHCFLLRTGMVHCLSEIELLAIIFAAAHHDYEHTGTTNSPHIQT 276
QY 259 KSECAIYVNDRSVLENHHSVFLMDDDMNIFINLTDEFFELRALVTEMVLATDMSC 318
DB 277 KSECAIYVNDRSVLENHHSVFLMDDDMNIFINLTDEFFELRALVTEMVLATDMSC 336
QY 319 HFQOVKMTALQOQLERIDPKKALSLLLHAADISHPTKQWLHVSRTWKALMEEFFRQGD 378
DB 337 HFQOVKMTALQOQLERIDPKKALSLLLHAADISHPTKQWLHVSRTWKALMEEFFRQGD 396
QY 379 EAEGLPSPCLCDRTSTLVAQSQIGFDIFVEPTFSVLTDAEKSVOPLADEDSKSNQP 438
DB 397 EAEGLPSPCLCDRTSTLVAQSQIGFDIFVEPTFSVLTDAEKSVOPLADEDSKSNQP 456
QY 439 SFOWRQPSLDVEGDPNDPVVSRSTWVKRIQENKQWKERRAASGITNQMIDELSPCEE 498
DB 457 SFOWRQPSLDVEGDPNDPVVSRSTWVKRIQENKQWKERRAASGITNQMIDELSPCEE 516
QY 499 EAPPSPAEDEHNGNGLD 516
DB 517 EAPPSPAEDEHNGNGLD 534

RESULT 3

US-08-297-494-27
Sequence 27, Application US/08297494
Patent No. 5580771

GENERAL INFORMATION:

APPLICANT: Beavo, Joseph A.
APPLICANT: Bentley, Kelley
APPLICANT: Charbonneau, Harry
APPLICANT: Sonnenburg, William K.
TITLE OF INVENTION: DNA Encoding Mammalian
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:

Db 397 EAEGLPSPCLDRTSTLVAQSIGDFIVETFSVLTDAEKSQPTGDDDSKKNQ 456
QY 439 SFOWRQPSLDVEGDPNDVVSFRSTWVKRIQENKOKWKERAASGITNOMSIDELSPCEE 498
Db 457 SFOWRQPSLDVEGDPNDVVSFRSTWVKRIQENKOKWKERAASGITNOMSIDELSPCEE 516
QY 499 EAPPSPAEHNQNGNLD 516
Db 517 EAPASPAEHNQNGNLD 534
RESULT 5
US-08-479-532-27
; Sequence 27, Application US/08479532
; Patent No. 5776752
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; TITLE OF INVENTION: Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; STREET: Two First National Plaza, 20 South Clark
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,532
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/297,494
; FILING DATE:
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5776752and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 534 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-479-532-27
Query Match 92.8%; Score 2484.5; DB 1; Length 534;
Best Local Similarity 96.0%; Pred. No. 4.9e-235;
Matches 478; Conservative 10; Mismatches 9; Indels 1; Gaps 1;
QY 19 LRYMKQLENGGINTEELKKNLEYTASLLEAVYIDETROIILDEQLRLSDAVPSEVR 78
Db 38 LRYMKQLENGGINTEELKKNLEYTASLLEAVYIDETROIILDEQLRLSDAVPSEVR 97
QY 79 DMLASTFTQOARAKGRRAEKEPKFRSIVHAVQAGIFVERMFRRTYTSVGPYSTAVLNCL 138
|||||

Db 98 DMLASTFTQOARAKG-PSEKPKFRSIVHAVQAGIFVERMFRRTYTSVGPYSTAVLNCL 156
QY 139 KNLDWCDFVSLNQADDDHALRTTVFELLTRHNLISRFKIPTVFLMSFLDALETGYGKY 198
Db 157 KNVDWCDFVSLNQADDDHALRTTVFELLTRHNLISRFKIPTVFLMTFLDALETGYGKY 216
QY 199 KNPYHNQIHAADVTQVHCFLLRRTGMVHCLSEIELLAIIFAAAIHDYEHGTGTTNSFHIQT 258
Db 217 KNPYHNQIHAADVTQVHCFLLRRTGMVHCLSEIELLAIIFAAAIHDYEHGTGTTNSFHIQT 276
QY 259 KSECAIVYNDRSVLENHHISSVFERLMQDDENNIFNLTKDFEVLRLVIEMLVATDMSC 318
Db 277 KSECAILYNDRSVLENHHISSVFERMQDDENNIFNLTKDFEVLRLVIEMLVATDMSC 336
QY 319 HFOOVKTKTALQOLERIDKPKALSLHLLHAADISHPTKOWLVHSHWTKALMEEPFGODK 378
Db 337 HFOOVKSMKTALQOLERIDKSKALSLHLLHAADISHPTKOWSVHSHWTKALMEEPFGODK 396
QY 379 EAEGLPSPCLDRTSTLVAQSIGDFIVETFSVLTDAEKSQPTGDDDSKKNQ 438
Db 397 EAEGLPSPCLDRTSTLVAQSIGDFIVETFSVLTDAEKSQPTGDDDSKKNQ 456
QY 439 SFOWRQPSLDVEGDPNDVVSFRSTWVKRIQENKOKWKERAASGITNOMSIDELSPCEE 498
Db 457 SFOWRQPSLDVEGDPNDVVSFRSTWVKRIQENKOKWKERAASGITNOMSIDELSPCEE 516
QY 499 EAPPSPAEHNQNGNLD 516
Db 517 EAPASPAEHNQNGNLD 534
RESULT 6
US-08-455-526-27
; Sequence 27, Application US/08455526
; Patent No. 5789553
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; TITLE OF INVENTION: Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; CITY: Street
; STATE: Chicago
; COUNTRY: Illinois
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,526
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9S 08/297,494
; FILING DATE: 29-AUG-1994
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5789553and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740

TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 534 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-455-526-27

Query Match 92.8%; Score 2484.5; DB 1; Length 534;
Best Local Similarity 96.0%; Pred. No. 4.9e-235;
Matches 478; Conservative 10; Mismatches 9; Indels 1; Gaps 1;
QY 19 LRYMVKQLENGEINTEELKKNLEYTASLLEAVYIDETROIQLDTEDELQELRSDAVPSEVR 78
Db LRYMVKQLENGEINTEELKKNLEYTASLLEAVYIDETROIQLDTEDELQELRSDAVPSEVR 97
QY 79 DWLASTFTQOARAKGRABEKPFRSIVHAVQAGIFVERMFRRTYTSVGPITYSTAVLNCL 138
Db DWLASTFTQOARAKGRABEKPFRSIVHAVQAGIFVERMFRRTYTSVGPITYSTAVLNCL 156
QY 139 KNLDLWCDFVSLNQAADHALRTIVFELLTRHNLISRPKIPTVFLMSFLDALETGYGY 198
Db KNLDLWCDFVSLNQAADHALRTIVFELLTRHNLISRPKIPTVFLMSFLDALETGYGY 216
QY 157 KNVDLWCDFVSLNQAADHALRTIVFELLTRHNLISRPKIPTVFLMTFLDALETGYGY 258
Db KNVDLWCDFVSLNQAADHALRTIVFELLTRHNLISRPKIPTVFLMTFLDALETGYGY 276
QY 199 KNPYHNQIHAADVTVCHFLRTGMVHCLSEIELLAIIFAAAIHDYEHGTGTTNSFHQT 318
Db KNPYHNQIHAADVTVCHFLRTGMVHCLSEIELLAIIFAAAIHDYEHGTGTTNSFHQT 336
QY 259 KSECAIVYNDRSVLENHHISSVFRMLQDDNMIFNLTKDEFVELRALVIEMLVATDMS 378
Db KSECAIVYNDRSVLENHHISSVFRMLQDDNMIFNLTKDEFVELRALVIEMLVATDMS 396
QY 379 EAELGLPSPCLDRSTSLVAQSIGIFDIFVEPTFSLTDAEKSQVQPLADSDSKNOP 438
Db EAELGLPSPCLDRSTSLVAQSIGIFDIFVEPTFSLTDAEKSQVQPLADSDSKNOP 456
QY 439 SFQWRQPSLDVEGDPNDVVSFRSTWVKRIQENKQKWKERAASGITNOMSIDELSPCEE 498
Db SFQWRQPSLDVEGDPNDVVSFRSTWVKRIQENKQKWKERAASGITNOMSIDELSPCEE 516
QY 499 EAPSPAEDHNQNGNLD 516
Db EAPSPAEDHNQNGNLD 534

RESULT 7
US-08-455-525-27
; Sequence 27, Application US/08455525
; Patent No. 5800987
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,525
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/297,494
FILING DATE:
APPLICATION NUMBER: US 07/688,356
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5800987and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30822
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 534 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-455-525-27
Query Match 92.8%; Score 2484.5; DB 1; Length 534;
Best Local Similarity 96.0%; Pred. No. 4.9e-235;
Matches 478; Conservative 10; Mismatches 9; Indels 1; Gaps 1;
QY 19 LRYMVKQLENGEINTEELKKNLEYTASLLEAVYIDETROIQLDTEDELQELRSDAVPSEVR 78
Db LRYMVKQLENGEINTEELKKNLEYTASLLEAVYIDETROIQLDTEDELQELRSDAVPSEVR 97
QY 79 DWLASTFTQOARAKGRABEKPFRSIVHAVQAGIFVERMFRRTYTSVGPITYSTAVLNCL 138
Db DWLASTFTQOARAKGRABEKPFRSIVHAVQAGIFVERMFRRTYTSVGPITYSTAVLNCL 156
QY 139 KNLDLWCDFVSLNQAADHALRTIVFELLTRHNLISRPKIPTVFLMSFLDALETGYGY 198
Db KNLDLWCDFVSLNQAADHALRTIVFELLTRHNLISRPKIPTVFLMTFLDALETGYGY 216
QY 157 KNPYHNQIHAADVTVCHFLRTGMVHCLSEIELLAIIFAAAIHDYEHGTGTTNSFHQT 258
Db KNPYHNQIHAADVTVCHFLRTGMVHCLSEIELLAIIFAAAIHDYEHGTGTTNSFHQT 276
QY 259 KSECAIVYNDRSVLENHHISSVFRMLQDDNMIFNLTKDEFVELRALVIEMLVATDMS 318
Db KSECAIVYNDRSVLENHHISSVFRMLQDDNMIFNLTKDEFVELRALVIEMLVATDMS 336
QY 379 EAELGLPSPCLDRSTSLVAQSIGIFDIFVEPTFSLTDAEKSQVQPLADSDSKNOP 438
Db EAELGLPSPCLDRSTSLVAQSIGIFDIFVEPTFSLTDAEKSQVQPLADSDSKNOP 456
QY 439 SFQWRQPSLDVEGDPNDVVSFRSTWVKRIQENKQKWKERAASGITNOMSIDELSPCEE 498
Db SFQWRQPSLDVEGDPNDVVSFRSTWVKRIQENKQKWKERAASGITNOMSIDELSPCEE 516
QY 499 EAPSPAEDHNQNGNLD 516
Db EAPSPAEDHNQNGNLD 534
RESULT 8
US-09-139-491-27
; Sequence 27, Application US/09139491
; Patent No. 6015677

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1  FILING DATE: 04-APR-1991
2  ATTORNEY/AGENT INFORMATION:
3  NAME: Noland, Greta E.
4  REGISTRATION NUMBER: 35,302
5  REFERENCE/DOCKET NUMBER: 27866/30822
6  TELECOMMUNICATION INFORMATION:
7  TELEPHONE: (312) 346-5750
8  TELEFAX: (312) 984-9740
9  TELEX: 25-3856
10 INFORMATION FOR SEQ ID NO: 27:
11     SEQUENCE CHARACTERISTICS:
12     LENGTH: 534 amino acids
13     TYPE: AMINO ACID
14     TOPOLOGY: linear
15     MOLECULE TYPE: protein
16     PCT-US92-0322:27
17
18     Query Match          92.8%   Score 2484.5;   DB 5;   Length 534;
19     Best Local Similarity 96.0%   Pred. No. 4.9e-235;
20     Matches 47%;   Conservative 10;   Mismatches 9;   Indels 1;   Gaps
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QY 79 DMLASTFTQARAKGRABEKPFRSIVHVAQIGFVERFMFRRTYSVGTYSSTAVLNCL 138
Db 98 DMLASTFTQTRAKG-PSEKPKFRSIVHVAQIGFVERFMFRRTYSVGTYSSTAVLNCL 156
QY 139 KNDLWCFDVSINQAADHALRTIVFELLTRHNLISREKPIPTVFLMSFLDALETGYKY 198
Db 157 KNVDLWCFDVSINRAADHALRTIVFELLTRHNLISREKPIPTVFLMTFLDALETGYKY 216
QY 199 KNPYHNOIHAADVTQVHCFLLRTGMVHCLSETELLAIIFAAAIHDEYHGTNTNSPHIOT 258
Db 217 KNPYHNOIHAADVTQVHCFLLRTGMVHCLSETELLAIIFAAAIHDEYHGTNTNSPHIOT 276
QY 259 KSECAIYVNDRSVLENHHSVFLRMQDDMMIFINLTKDEFVELRALVEMVLATDMSC 318
Db 277 KSECAIYVNDRSVLENHHSVFLRMQDDMMIFINLTKDEFVELRALVEMVLATDMSC 336
QY 319 HFQOVKMTALQQLERIDKPKALSLLHAADISHPTKOWLVHSRWTKALMEEFFRQGD 378
Db 337 HFQOVKSMKTALQQLERIDKPKALSLLHAADISHPTKOWLVHSRWTKALMEEFFRQGD 396
QY 379 EAEGLPFPPLCDRTSTLVAQOIGFIDFIVEPTESVLTDAEKSQPLADEDSKSNOP 438
Db 397 EAEGLPFPPLCDRTSTLVAQOIGFIDFIVEPTESVLTDAEKSQPLADEDSKSNOP 456
QY 439 SFQWRQPSLDVEGDPNPDVFSFRSTWVKRIQENKOKKERAASGITNOMSIDELSPCEE 498
Db 457 SFQWRQPSLDVEGDPNPDVFSFRSTWVKRIQENKOKKERAASGITNOMSIDELSPCEE 516
QY 499 EAPPSPADEHNQNGNLD 516
Db 517 EAPPSPADEHNQNGNLD 534

RESULT 10

US-07-872-644-17
; Sequence 17, Application US/07872644
; Patent No. 5389527
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; TITLE OF INVENTION: Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/872,644
; FILING DATE: 19920420
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5389527and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740

; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 514 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-872-644-17

Query Match 61.2%; Score 1636.5; DB 1; Length 514;
Best Local Similarity 60.8%; Pred. No. 7.2e-152;
Matches 309; Conservative 94; Mismatches 96; Indels 9; Gaps 1;

QY 1 MANPVPQVSHLQGPILRLRYMYKQLENGEINTEELKKNLEYASLEAVYIDETQIILD 60
Db 1 MDHVTIRKHLQRPFRRLKCLVQLEKGDVNVIDLKKNIEYAASLEAVYIDETRLLD 60
QY 61 TEDELQELSDAVPSEVRDMLASTFTQARAKGRABEKPFRSIVHVAQIGFVERMFR 120
Db 61 TDDELSDIQSDSVSEVRDMLASTFTQARAKGRABEKPFRSIVHVAQIGFVERMYR 120
QY 121 RYTSVGPYSTAVLNCLNLDLWCFDVSINQAADHALRTIVFELLTRHNLISREKPI 180
Db 121 KSYHMYGLAYPEAVIIVTLKDVKWSFDVFNALNEASGEHSLKFWIELFTRYDLINRFPKIP 180
QY 181 TVFLMSFLDALETGYKYNPNYHNOIHAADVTQVHCFLLRTGMVHCLSETELLAIIFAA 240
Db 181 VSLCIAFAEALEVGYSKYNPNYHNOIHAADVTQVHIMLHTGIMHMLTELEILAMVFAA 240
QY 241 AIHDEYHGTNTNSPHIOTKSECAIYVNDRSVLENHHSVFLRMQDDMMIFINLTKDEF 300
Db 241 AIHDEYHGTNTNSPHIOTKSECAIYVNDRSVLENHHSVFLRMQDDMMIFINLTKDEF 300
QY 301 VELRALVEMVLATDMSCHFQOVKMTALQQLERIDKPKALSLLHAADISHPTKOWLV 360
Db 301 RDLNLVEMVLSTDMSGHFQOVKMTALQQLERIDKPKALSLLHAADISHPTKOWLV 360
QY 361 HSRWTKALMEEFFRQGDKEAELGLPFPPLCDRTSTLVAQOIGFIDFIVEPTESVLTDA 420
Db 361 HSRWTKALMEEFFRQGDKEAELGLPFPPLCDRTSTLVAQOIGFIDFIVEPTESVLTDA 420
QY 421 EKSQVPLADEDSKSNOPSFQWRQPSLDVEGDP-----PNPDVVSFRSTWVKRIQE 471
Db 421 EKIIIPLEEDSKTKTPSYCASRRSNMKGTTNDGTYSPTYSLASVDLKFKNLSLVDIQ 480
QY 472 NKQWKERAASGITNOMSIDELSPCEE 499
Db 481 NKERWKEAAGPEPDHPKNSDLVNAEEK 508

RESULT 11

US-08-297-494-17
; Sequence 17, Application US/08297494
; Patent No. 5580771
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; TITLE OF INVENTION: Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
TITLE OF INVENTION: Phosphodiesterases
NUMBER OF SEQUENCES: 58
FILING DATE: US/08/297,494
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/688,356
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: NO. 558077land, Greta E.
REGISTRATION/DOCKET NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30822
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 514 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-297-494-17

Query Match 61.2%; Score 1636.5; DB 1; Length 514;
Best Local Similarity 60.8%; Pred. No. 7.2e-152;
Matches 309; Conservative 94; Mismatches 96; Indels 9; Gaps 1;

Qy 1 MANPVPORSHLOQPILRLRYMYKQLENGEINIEELKKNLEYTASLEAVYIDETRLD 60
Db 1 MDDHVTIRKHLQRPILRLCLYKQLEKGVNIDLNKNEYAASVLEAVYIDETRLD 60
Qy 61 TEDELQELSDAVSEVROWLASTFTQOARAKGRRAEERPKFRSIVHVAQAGIFVERMR 120
Db 61 TDELSDIQSDSPSEVROWLASTFTFRKMGMMKKSEKPRFRSIVHVAQAGIFVERMR 120
Qy 121 RYTSVGYPTSTAVLNCNKLNDLWCFDVSFNQAADHALRTIVFELLTRHNLISRFKIP 180
Db 121 KSYHVMGLAYPEAVIVTLKDVKWSFDVFALNEASGEHSLKFMIELEFTRYDLINRFKIP 180
Qy 181 TVFLMSFLDALETGYGKYKNPYHNOIHAADVTQTVHCFLLRTGMVHCLSEIELLAIFAA 240
Db 181 VSCLIAPAEALVEGYSKYKNPYHNLIIHAADVTQTVHIMLTGIMHMLTELEILAMVFAA 240
Qy 241 AIHDEYHTGTNSFHIQTKSECAIVYNDRSVLENHHISSVFRMLQDDEMNIFNLTKDEF 300
Db 241 AIHDEYHTGTNNFHIQTRSDVAILYNDRSVLENHHVSAAYRLMQEEMNVLINLSKDDW 300
Qy 301 VELRALVIEMLATDMSCHFOQVKTMTALQQLERIDKPKALSLLLHAADISHPTKOWLV 360
Db 301 RDLNRLVIEMLVSTDMSGHFQOIKNIRNSLQOPEGLDKAKTMSLILHAADISHPAKSWKL 360
Qy 361 HSRWTKALMEEFFROGDKAEGLPSPICDRTSTLVAQSQIGFIDFIVEPTFSVLTDA 420
Db 361 HHRWTALMEEFFROGDKAEGLPSPICDRTSTLVAQSQIGFIDFIVEPTFSVLTST 420
Qy 421 EKSQVPLADRSKSNQPSQFWRQPSLDVEVG-----PNDVVSFRSTWVRKIOE 471
Db 421 EKIIPLIEDSKTKTPSYGASRRSNMKTGNTDGTSPDYSLASVLDKSKFNLSVDIIQO 480
Qy 472 NKQWKERAASGITNQMSIDELSPCEEE 499
Db 481 NKERWKELAQGPDPKHNKSDLVNAEEK 508

RESULT 12
US-08-297-510-17
Sequence 17, Application US/08297510
Patent No. 5602019
GENERAL INFORMATION:
APPLICANT: Beavo, Joseph A.

APPLICANT: Bentley, Kelley
APPLICANT: Charbonneau, Harry
APPLICANT: Sonnenburg, William K.
TITLE OF INVENTION: DNA Encoding Mammalian
Phosphodiesterases
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
STREET: Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/08/297,510
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/688,356
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5602019and, Greta E.
REGISTRATION/DOCKET NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30822
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 514 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-297-510-17

Query Match 61.2%; Score 1636.5; DB 1; Length 514;
Best Local Similarity 60.8%; Pred. No. 7.2e-152;
Matches 309; Conservative 94; Mismatches 96; Indels 9; Gaps 1;

Qy 1 MANPVPORSHLOQPILRLRYMYKQLENGEINIEELKKNLEYTASLEAVYIDETRLD 60
Db 1 MDDHVTIRKHLQRPILRLCLYKQLEKGVNIDLNKNEYAASVLEAVYIDETRLD 60
Qy 61 TEDELQELSDAVSEVROWLASTFTQOARAKGRRAEERPKFRSIVHVAQAGIFVERMR 120
Db 61 TDELSDIQSDSPSEVROWLASTFTFRKMGMMKKSEKPRFRSIVHVAQAGIFVERMR 120
Qy 121 RYTSVGYPTSTAVLNCNKLNDLWCFDVSFNQAADHALRTIVFELLTRHNLISRFKIP 180
Db 121 KSYHVMGLAYPEAVIVTLKDVKWSFDVFALNEASGEHSLKFMIELEFTRYDLINRFKIP 180
Qy 181 TVFLMSFLDALETGYGKYKNPYHNOIHAADVTQTVHCFLLRTGMVHCLSEIELLAIFAA 240
Db 181 VSCLIAPAEALVEGYSKYKNPYHNLIIHAADVTQTVHIMLTGIMHMLTELEILAMVFAA 240
Qy 241 AIHDEYHTGTNSFHIQTKSECAIVYNDRSVLENHHISSVFRMLQDDEMNIFNLTKDEF 300
Db 241 AIHDEYHTGTNNFHIQTRSDVAILYNDRSVLENHHVSAAYRLMQEEMNVLINLSKDDW 300
Qy 301 VELRALVIEMLATDMSCHFOQVKTMTALQQLERIDKPKALSLLLHAADISHPTKOWLV 360
Db 301 RDLNRLVIEMLVSTDMSGHFQOIKNIRNSLQOPEGLDKAKTMSLILHAADISHPAKSWKL 360
Qy 361 HSRWTKALMEEFFROGDKAEGLPSPICDRTSTLVAQSQIGFIDFIVEPTFSVLTDA 420
Db 361 HHRWTALMEEFFROGDKAEGLPSPICDRTSTLVAQSQIGFIDFIVEPTFSVLTST 420

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Db 361 HHRWTMALWEEFFLQGDKEAELGLPSPCLDRKSTWVAQSIGFIDFIVEPTFSLTDTST 420
Qy 421 EKSVOPLADESKSNQPSFQWRQPSLDVEVGD-----PNPDVVSFRSTWVKRQIE 471
Db 421 EKIIPLIEEDSKTKTPSYGASRRSNMKGTTNDGTYSPTYSLASVDLAKSFKNLSVDIIQQ 480
Qy 472 NQKWKERAASGITNOMSIDELSPCEE 499
Db 481 NKRWKEAAGEPDPHKNSDLVNAEK 508

RESULT 13
US-08-479-532-17
; Sequence 17, Application US/08479532
; Patent No. 5776752
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,532
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/297,494
; FILING DATE: 04-APR-1991
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5776752and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 514 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-479-532-17

Query Match 61.2%; Score 1636.5; DB 1; Length 514;
Best Local Similarity 60.8%; Pred. No. 7.2e-152;
Matches 309; Conservative 94; Mismatches 96; Indels 9; Gaps 1;

Qy 1 MANPVQSRHQGLPILRYVMVKOLENGEINIEELKKNLEYTASLLBAVYIDETRQILD 60
Db 1 MDDHTVIRKHLQRFIFRLCLVQKLEGDVNDLKKNIETAAVSLVLEAVYIDETRRLD 60
Qy 61 TEDELQELRSDAVSEVRDLASTFTQARAKGRRAEKKPKFRSTVHVAVQAGIFVERMF 120
Db 61 TDELSLDQSDSVSEVRDLASTFTTRKGMWKKSEKKPKFRSTVHVAVQAGIFVERMYR 120
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INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 514 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-455-526-17

Query Match 61.2%; Score 1636.5; DB 1; Length 514;
Best Local Similarity 60.8%; Pred. No. 7.2e-152;
Matches 309; Conservative 94; Mismatches 96; Indels 9; Gaps 1;

QY 1 MANPVQVSHLQGLPILRLRYMVKOLENGEINIEELKKNLEYTASLEAVYIDETRIQLD 60
Db 1 MDDHVTIRKKHLQRIPLRCLVKOLEKGVNVDLKNIEYAASVLEAVYIDETRIQLD 60
QY 61 TEDELQELSDAVPSVSEVRDLASTFTQQAARAKGRRAEKKPKPRSIHVAVQAGIFVERMYR 120
Db 61 TDELDSDIQSDSPSEVRDLASTFTQQAARAKGRRAEKKPKPRSIHVAVQAGIFVERMYR 120
QY 121 RTYTSVGYPTYSTAVLNCLNLDLWCFDVFSLNQAAADHALRTIVFELLTRHNLISRFKIP 180
Db 121 KSYHVMGLAYPEAVITLKDVKWDFVFNALNEASGEHSLKPMIYELFTRYDLINRFKIP 180
QY 181 TVFLMSFLDALETGYCKYKNPYHNOIHAADVDTQTVHCTVHCLSEIALLAIIFAA 240
Db 181 VSLIAFAEALEVGYSKYKNPYHNLIIHAADVDTQTVHCTVHCLSEIALLAIIFAA 240
QY 241 AIHDYEHTGTTNSPHIOTKSECAIVYNDRSVLENHHISSVFLRMQDDENFINLTKDEF 300
Db 241 AIHDYEHTGTTNNPHIOTKSECAIVYNDRSVLENHHISSVFLRMQDDENFINLTKDEF 300
QY 301 VELRALVIEVLATDMSCHFOQVTKMTALQOLERIDKPKALSLLLHAADISHPTKQWLV 360
Db 301 RDLRLNVIEMVLSTDMSGHFOQVTKMTALQOLERIDKPKALSLLLHAADISHPTKQWLV 360
QY 361 HSRWTKALMEEFPRQGDKEALGLPFLCDRTSTLVAOSQIGFIDFIVEPTFSLTDT 420
Db 361 HHRWTALMEEFPRQGDKEALGLPFLCDRTSTLVAOSQIGFIDFIVEPTFSLTDT 420
QY 421 EKSQVPLADEDSKSNQPSFQWRQPSLDVEVGD-----PNDPVVSFRSTWVKRQOE 471
Db 421 EKIIPLIEEDSKTKPSYGASRRSNMKGTTNDGTYSPTYSLASVLDKSKNSLVDIIQQ 480
QY 472 NKQWKERAASGITNQMSIDELSPCEE 499
Db 481 NKERWELAAQGEPPHKNSDLVNAEEK 508

RESULT 15
US-08-455-525-17
Sequence 17, Application US/08455525
Patent No. 5800987
GENERAL INFORMATION:
APPLICANT: Beavo, Joseph A.
APPLICANT: Bentley, Kelley
APPLICANT: Charbonneau, Harry
APPLICANT: Sonnenburg, William K.
TITLE OF INVENTION: DNA Encoding Mammalian
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell, 20 South Clark
STREET: Two First National Plaza, 20 South Clark
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,525
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/297,494
FILING DATE:
APPLICATION NUMBER: US 07/688,356
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5800987and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30822
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 514 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-455-525-17

Query Match 61.2%; Score 1636.5; DB 1; Length 514;
Best Local Similarity 60.8%; Pred. No. 7.2e-152;
Matches 309; Conservative 94; Mismatches 96; Indels 9; Gaps 1;

QY 1 MANPVQVSHLQGLPILRLRYMVKOLENGEINIEELKKNLEYTASLEAVYIDETRIQLD 60
Db 1 MDDHVTIRKKHLQRIPLRCLVKOLEKGVNVDLKNIEYAASVLEAVYIDETRIQLD 60
QY 61 TEDELQELSDAVPSVSEVRDLASTFTQQAARAKGRRAEKKPKPRSIHVAVQAGIFVERMYR 120
Db 61 TDELDSDIQSDSPSEVRDLASTFTQQAARAKGRRAEKKPKPRSIHVAVQAGIFVERMYR 120
QY 121 RTYTSVGYPTYSTAVLNCLNLDLWCFDVFSLNQAAADHALRTIVFELLTRHNLISRFKIP 180
Db 121 KSYHVMGLAYPEAVITLKDVKWDFVFNALNEASGEHSLKPMIYELFTRYDLINRFKIP 180
QY 181 TVFLMSFLDALETGYCKYKNPYHNOIHAADVDTQTVHCTVHCLSEIALLAIIFAA 240
Db 181 VSLIAFAEALEVGYSKYKNPYHNLIIHAADVDTQTVHCTVHCLSEIALLAIIFAA 240
QY 241 AIHDYEHTGTTNSPHIOTKSECAIVYNDRSVLENHHISSVFLRMQDDENFINLTKDEF 300
Db 241 AIHDYEHTGTTNNPHIOTKSECAIVYNDRSVLENHHISSVFLRMQDDENFINLTKDEF 300
QY 301 VELRALVIEVLATDMSCHFOQVTKMTALQOLERIDKPKALSLLLHAADISHPTKQWLV 360
Db 301 RDLRLNVIEMVLSTDMSGHFOQVTKMTALQOLERIDKPKALSLLLHAADISHPTKQWLV 360
QY 361 HSRWTKALMEEFPRQGDKEALGLPFLCDRTSTLVAOSQIGFIDFIVEPTFSLTDT 420
Db 361 HHRWTALMEEFPRQGDKEALGLPFLCDRTSTLVAOSQIGFIDFIVEPTFSLTDT 420
QY 421 EKSQVPLADEDSKSNQPSFQWRQPSLDVEVGD-----PNDPVVSFRSTWVKRQOE 471
Db 421 EKIIPLIEEDSKTKPSYGASRRSNMKGTTNDGTYSPTYSLASVLDKSKNSLVDIIQQ 480
QY 472 NKQWKERAASGITNQMSIDELSPCEE 499
Db 481 NKERWELAAQGEPPHKNSDLVNAEEK 508

Search completed: August 11, 2003, 01:13:38
Job time : 45 secs

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OM protein - protein search, using sw model

Run on: August 11, 2003, 01:11:57 ; Search time 337 Seconds
(without alignments)
181.840 Million cell updates/sec

Title: US-09-663-481-1

Perfect score: 2676

Sequence: 1 MANPVPVQRSHLQPIILRLR.....EEEAAPPSPAEHNGNGLD 516

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 451899 seqs, 118759770 residues

Total number of hits satisfying chosen parameters: 451899

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications_AA:*

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- 3: /cgn2_6/ptodata/2/pubpaa/US05_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
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- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2484.5	92.8	534	10	US-09-883-825-27
2	1636.5	61.2	514	10	US-09-883-825-17
3	1593	59.5	634	10	US-09-883-825-51
4	1591.5	59.5	530	10	US-09-883-825-6
5	1568.5	58.6	535	10	US-09-883-825-49
6	1206	45.1	564	10	US-09-883-825-53
7	668	25.0	137	10	US-09-883-825-23
8	626	23.4	712	15	US-10-076-597-47
9	622.5	23.3	585	15	US-10-076-514-9
10	617.5	23.1	507	15	US-10-076-597-49
11	617.5	23.1	507	15	US-10-067-514-10
12	617.5	23.1	673	15	US-10-076-597-51
13	617.5	23.1	673	15	US-10-067-514-6
14	617.5	23.1	687	15	US-10-067-514-8
15	617.5	23.1	745	15	US-10-076-597-50

16	617.5	23.1	745	15	US-10-067-514-4
17	617.5	23.1	809	15	US-10-067-514-2
18	617.5	22.9	647	15	US-10-076-597-46
19	610.5	22.8	564	9	US-09-947-305-2
20	610.5	22.8	564	15	US-10-076-597-48
21	603.5	22.6	584	9	US-09-802-741A-4
22	464	17.3	426	11	US-09-966-781A-2
23	461.5	17.2	426	11	US-09-966-781A-3
24	457.5	17.1	426	11	US-09-966-781A-1
25	435.5	16.8	713	9	US-09-802-741A-3
26	435.5	15.8	432	9	US-09-764-898-208
27	405	15.1	580	15	US-10-083-620A-21
28	405	15.1	593	9	US-09-802-741A-1
29	403.5	15.1	533	15	US-10-083-620A-19
30	403	15.1	466	15	US-10-083-620A-2
31	390.5	14.6	320	15	US-10-083-620A-17
32	373.5	14.0	285	11	US-09-989-442-94
33	338	12.6	490	15	US-10-094-168B-1
34	338	12.6	576	10	US-09-891-216-13
35	338	12.6	684	10	US-09-891-216-14
36	338	12.6	934	10	US-09-891-216-12
37	338	12.6	934	10	US-09-891-216-15
38	336.5	12.6	905	14	US-10-094-989-4
39	336.5	12.6	920	14	US-10-094-989-2
40	336.5	12.6	941	10	US-09-883-825-45
41	335.5	12.5	921	10	US-09-883-825-39
42	335.5	12.5	921	14	US-10-094-989-5
43	335.5	12.5	942	10	US-09-883-825-43
44	319.5	11.9	211	9	US-09-764-898-280
45	319.5	11.9	211	11	US-09-989-442-120

ALIGNMENTS

RESULT 1

US-09-883-825-27
; Sequence 27, Application US/09883825
; Patent No US20020151024A1
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; Bentley, Kelley
; Charbonneau, Harry
; Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; Bicknell
; STREET: Two First National Plaza, 20 South Clark
; Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/883,825
; FILING DATE: 18-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIORITY INFORMATION:
; APPLICATION NUMBER: 09/123,783
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/297,494
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:

NAME: No. US20020151024Aland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30822
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 534 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-09-883-825-27

Query Match 92.8%; Score 2484.5; DB 10; Length 534;
Best Local Similarity 96.0%; Pred. No. 7.5e-233;
Matches 478; Conservative 10; Mismatches 29; Indels 1; Gaps 1;

QY 19 LRYMVKQLENGEINIEELKNLEYTASLLEAVYIDETQILDTDEQLRLSDAVPSEVR 78
Db 38 LRYMVKQLENGEINIEELKNLEYTASLLEAVYIDETQILDTDEQLRLSDAVPSEVR 97
QY 79 DLWLASTFOQARAKGRRAEKPFRSIVHVAQAGIEVERMFRRTYTSVGTPTYSTAVLNCL 138
Db 98 DLWLASTFOQTRAKG-PSEKPKFRSIVHVAQAGIEVERMFRRTYTSVGTPTYSTAVLNCL 156
QY 139 KNLDLWCFDVFSLNQADHALRTIVFELLTRHNLISREFKIPTVFLMSFLDALETGYGY 198
Db 157 KNVDLWCFDVFSLNRAADHALRTIVFELLTRHNLISREFKIPTVFLMFLDALETGYGY 216
QY 199 KNPYHQIHAADVTQVHGFLLRTGMVHCLSELELLAIFAAAIHDYHTGTTNSFHOT 258
Db 217 KNPYHQIHAADVTQVHGFLLRTGMVHCLSELELLAIFAAAIHDYHTGTTNSFHOT 276
QY 259 KSCALVYNDRSVLENNHSSVFLRMQDDMMNIFNLTKDEFVELRALVEMVLATDMSC 318
Db 277 KSCALVYNDRSVLENNHSSVFLRMQDDMMNIFNLTKDEFVELRALVEMVLATDMSC 336
QY 319 HFQOQVMTALQOOLERIDPKKALSLLLHAADISHTPKOMLVHRSWTKALMEEFPRQGD 378
Db 337 HFQOQVMTALQOOLERIDPKKALSLLLHAADISHTPKOMLVHRSWTKALMEEFPRQGD 396
QY 379 EAEGLPFPPLCDRTSTLVAQSQIGFIDFIVEPTFSLTDVAEKSVPQIADDESKSNOP 438
Db 397 EAEGLPFPPLCDRTSTLVAQSQIGFIDFIVEPTFSLTDVAEKSVPQIADDESKSNOP 456
QY 439 SFQWRQPSLDVEGDPNPDVWSFRSTWVKRIQENKQKWKERAASGITNMQSIDELSPCEE 498
Db 457 SFQWRQPSLDVEGDPNPDVWSFRSTWVKRIQENKQKWKERAASGITNMQSIDELSPCEE 516
QY 499 EAPPSPAEDEHNGNLD 516
Db 517 EAPPSPAEDEHNGNLD 534

RESULT 2
US-09-883-825-17
Sequence 17, Application US/09883825
Patent No. US20020151024A1
GENERAL INFORMATION:
APPLICANT: Beavo, Joseph A.
Bentley, Kelley
Charbonneau, Harry
Sonnenburg, William K.
TITLE OF INVENTION: DNA Encoding Mammalian
Phosphodiesterases
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESS: Marshall, O'Toole, Gerstein, Murray &
Bicknell
STREET: Two First National Plaza, 20 South Clark

Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/883,825
FILING DATE: 18-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/123,783
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/297,494
FILING DATE: <Unknown>
APPLICATION NUMBER: US 07/688,356
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. US20020151024Aland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30822
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 514 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-883-825-17

Query Match 61.2%; Score 1636.5; DB 10; Length 514;
Best Local Similarity 60.8%; Pred. No. 2.3e-150;
Matches 309; Conservative 94; Mismatches 96; Indels 9; Gaps 1;

QY 1 MANPYVORSHLQGPILRLRYMVKQLENGEINIEELKNLEYTASLLEAVYIDETQILDT 60
Db 1 MDHVTYIRKHLQRPFRRLCLVKOLEKGDVNVLDKKNIEYAASVLEAVYIDETRRLLD 60
QY 61 TEDELQELRSDAVPSEVRDNLASTFTQARAKGRRAEKPFRSIVHVAQAGIEVERMFR 120
Db 61 TDELSLDSIQSDSVSEVRDNLASTFTRKMGMMKKSEKPRFRSIVHVVQAGIEVERMYR 120
QY 121 RYTSVGTPTYSTAVLNCLNLDLWCFDVFSLNQADHALRTIVFELLTRHNLISREFKI 180
Db 121 KSYHMVGLAYPEAVIVTLKVDKWSFDVFALNEASGEHSLRFMIYELTRYDLINRKP 180
QY 181 TVFLMSFLDALETGYGYKNPYHQIHAADVTQVHGFLLRTGMVHCLSELELLAIFAA 240
Db 181 VSLIRFAEAELEVGYSKYNPYHNLHAADVTQVHYIMLHTGIMHWLEILLAWFAA 240
QY 241 AIHDYHTGTTNSFHOTKSECAIVYNDRSVLENNHSSVFLRMQDDMMNIFNLTKDEF 300
Db 241 AIHDYHTGTTNSFHOTKSECAIVYNDRSVLENNHSSVFLRMQDDMMNIFNLTKDEF 300
QY 301 VELRALVEMVLATDMSCHFQOQVMTALQOOLERIDPKKALSLLLHAADISHTPKOMLV 360
Db 301 IDLRNLVEMVLSTDMSCHFQOIKNIRNSLQOPEGLDKAKTMSLLHAADISHPAKSWKL 360
QY 361 ISRWTKALMEEFPRQGDKEAELGLPFPPLCDRTSTLVAQSQIGFIDFIVEPTFSLTDVA 420
Db 361 IHRWTMALMEEFPRQGDKEAELGLPFPPLCDRKSTWVAQSQIGFIDFIVEPTFSLTDST 420
QY 421 IKSVPQIADDESKSNOPSFQWRQPSLDVEGDPNPDVWSFRSTWVKRIQENKQKWKERA 471
Db 421 IKIIPLEEDSKTTPSYGASRRSNMKGTTNDGTYSYSLASVDLKSFKNSLVDIIQ 480


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; INFORMATION FOR SEQ ID NO: 6
; SEQUENCE CHARACTERISTICS:
; LENGTH: 530 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6
US-09-883-825-6

Query Match 59.5%; Score 1591.5; DB 10; Length 530;
Best Local Similarity 61.2%; Pred. No. 5.7e-146;
Matches 309; Conservative 91; Mismatches 90; Indels 9; Gaps 1;

QY 19 LRYVWVQLENGEINIEELKKNLEYTASLEAVYIDETQIOLDTEDELAELSDAVPSEVR 78
Db 35 LRLCVLQLEKGDVNVLDKKNIEYAAASVLEAVYIDETRLDLDDELSDIOSDVPSEVR 94
QY 79 DWLASTTQOARAKGRRAEKKPRFSIVHVAQAGIFVERMFRRTYTSVGPYSTAVLNCL 138
Db 95 DWLASTTFRKMGMTKKKPEEKPRFSIVHVAQAGIFVERMYRKYHMYGLAYPAIVITL 154
QY 139 KNLDLWCDFVSLNQAAADHALRTIVFELLRHNLISRFKIPVTFMFLSDALETGYGKY 198
Db 155 KDVKWKSDFVAFALNEASGEHSLKFMIEFLTRYDLINRFRKIPVSCLIATAFAEALEVGYSKY 214
QY 199 KNPYHNOIHAADVDTQVHCLGMVHCLSEIELLAIIFAAAIHDYEHTGTGTTNSFHQT 258
Db 215 KNPYHNLIIHAADVDTQVHIMLHTGIMHMLTELEILAMVFAAAIHDYEHTGTGTTNFHIQT 274
QY 259 KSCATVYNDRSVLENHHTSSVFLMDDMMNIFNLTKDEFVELRALVIEMLATDMSC 318
Db 275 RSDVAILYNDRSVLENHVSAAVRLMOEEMVNLNLSKDDWRDLNVLVIEMLVSTDMG 334
QY 319 HFQOVKMTALQOOLERIDPKKALLSLHHAADISHPTKQWLVSHTKALMEEFFROGDK 378
Db 335 HFQOIKNIRSLQOPEGIDIRAKTMSLLHHAADISHPAKSWKLYHMYRTMALMEEFFLOGDK 394
QY 379 EAEGLPFPPLCORTSTVLAQSQIGFDIVETPFTSVLTDVAEKSQVPLADEDSKKNOP 438
Db 395 EAEGLPFPPLCDRKSTVLAQSQIGFDIVETPFTSLTDSPEKIIILIBEDSKTKTPS 454
QY 439 SFQWRQPSLDVEGD-----PNPDVVSFRSTWVKRIQENKQKRAASGITNOMS 489
Db 455 YGASRRSNMKGTTNDGTSPDYSLASVDLKSFKNSLVLDIIQONKERKELAAQGPDPHK 514
QY 490 IDLSLPCREE 499
Db 515 NSDLVNAEEK 524

RESULT 5
; Sequence 49, Application US/09883825
; Patent No. US20020151024A1
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; Bentley, Kelley
; Charbonneau, Harry
; Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; Bicknell
; STREET: Two First National Plaza, 20 South Clark
; Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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US-09-883-825-53
; Sequence 53, Application US/09883825
; Patent No. US20020151024A1
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; Bentley, Kelley
; Charbonneau, Harry
; Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; Bicknell
; STREET: Two First National Plaza, 20 South Clark
; Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/883,825
; FILING DATE: 18-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/123,783
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/297,494
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20020151024A1and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 564 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 53:
US-09-883-825-53
Query Match 45.1%; Score 1206; DB 10; Length 564;
Best Local Similarity 57.9%; Pred. No. 2e-108;
Matches 237; Conservative 61; Mismatches 71; Indels 40; Gaps 5;
QY 121 RYTSVGTSTYAVLNCLNLDKCFDVFSLNQADHIALRTIVFELLTRHNLISRFKIP 180
Db 1 RTSNMVGSLSPYPAVTEALKDVKDFVSLNEASGDHALKFIFELLTRYDLISRFKIP 60
QY 181 TVFLMSFLDALFTGKYGKPNYHNOIHAADVTTQVHCFLRTGMVHCLSEIELLAIIPAA 240
Db 61 ISALVSFEALVEGVGSKHNPYHNLHMLHADVTQTVHYLLYKTVGVANLWLEIFALIFSA 120
QY 241 AIHDYEHTGTNTSFHIQTKSECAIYVNDRSVLENHHISVFRIMQDD-EMNFINLTKDE 299
Db 121 AIHDYEHTGTNTNFHIQTRSDPAIYNDRSVLENHLSAAAYRLQDDDEMNILNLSKDD 180
QY 300 FVELRALVTEMVLAIDMSCHFOQVTKMTALQOQLERIDKPKALSLLLHAADISHPTKOWL 359
Db 181 WREFRTLVIEMVMAIDMSCHFOQIKAMKTAQOQPEAIEKPKALSMLLHTADISHPAKAWD 240
QY 360 VHSRWTKALMEEFFRQGDKEAELGPFPLCDRTSLVAQSQIGFDIFVEFTFSLTVDV 419
Db 241 LHRWTMSLLEEFFRQGDREAEGLGPFPLCDRKSTWVAQSQVGFDFIVETFTVLTDM 300
QY 420 AKSVQPLADEDSKSNQPSFQWRQPSLD-VEVGDP-----NPD 457
Db 301 TEKIVSPLIDETSQTGGTQ---RRSSLNSISSDAKRSVKTSSEGSAPINNNSVISVD 357
QY 458 VVSFRSTWVKRIOENKQKWKERAAASGITNQMSIDELSPCEEAPPSPAE 506
Db 358 YKSFRAKTWTEVVHINRWRAKV-----PKERAKKEAEE 392
RESULT 7
US-09-883-825-23
; Sequence 23, Application US/09883825
; Patent No. US20020151024A1
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; Bentley, Kelley
; Charbonneau, Harry
; Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; Bicknell
; STREET: Two First National Plaza, 20 South Clark
; Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/883,825
; FILING DATE: 18-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/123,783
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/297,494
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20020151024A1and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 137 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-883-825-23
Query Match 25.0%; Score 668; DB 10; Length 137;
Best Local Similarity 93.4%; Pred. No. 4.9e-57;
Matches 128; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
QY 242 IHDYEHTGTNTSFHIQTKSECAIYVNDRSVLENHHISVFRIMQDDENHIFNLTKDEFV 301
Db 121 IHDYEHTGTNTNFHIQTRSDPAIYNDRSVLENHLSAAAYRLQDDDEMNILNLSKDD 180
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; LENGTH: 673
; TYPE: PRT

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; ORGANISM: human
US-10-076-597-51

Query Match
Best Local Similarity 23.1%; Score 617.5; DB 15; Length 673;
Matches 151; Conservative 105; Mismatches 174; Indels 75; Gaps 14;

QY 24 KOLENGEI-NIEELKKLEYTASLLLEAVYIDETROILDTDELEQLRSDAVPSEVDWLA 82
D 173 KRLNRELTHLSEMSRSGNOVSEFISNTFLDKQHEV-----EIPSP-----213
QY 83 STFTQARAKGR-AEEKPKFRSIVHVAQAGIFVERMFRRTYTSVGTYST-----AVL 135
D 214 ---TOKEKEKKRPMQISGVKKLMHSSSL-----TNSSI-PRFGVKTEQEDVLA 259
QY 136 NCLKNLDLWCFDVFSLNQADDAHALRTIVFELLTRNLNLSRFPKIPVFLMSFLDALETGY 195
D 260 KELEDVKNKGLHVFRIAELSGNRPLVIMHTIFQERDLTKFKIPVDTLITYLMTLEDHY 319
QY 196 GYKKNPYHNOIHAADVTQTVHCFLLRTGMVHCLSEIELLAIIPAAAIHDEYHTGTNSFH 255
D 320 -HADVAYHNNIHAADVQVSTHLLSTPALEAVFTDLEILAAIFASAIHVDVHFGVSNQFL 378
QY 256 IQTKSECAIYNDRSVLENHHISSVFLMDDMNIFINLTQDEFVELRALVTEMVLATD 315
D 379 INTNSELALYNDSSVLENHHAVGFKLQEECNDIFQNLTKKQOSLRKMWIDIVLATD 438
QY 316 MSCHFQOVKMTKTAQOLE-----RIDKPKALSLLLHAAIDISHPTKQWLHVRW 364
D 439 MSKHMNLLADLKTVMETKVTSSGVLLLDNYSDRIOVLQNMVHCADLSNPTKPLQYROW 498
QY 365 TKALMEEFFRQGDKEAELGLPFLCDRTSTLVAQSIGIFIDFIVEPTFSVLTDVAEKSV 424
D 499 TDRIMEEFFRQGDREMERGMEISPMCDKHNASVEKSGVGFIDYIVHPLWETWADLVHPDA 558
QY 425 QPLAD--EDSKSNQPSFQWRQPSLDVEGDPNDPVVSFRSTWVKRIQENKQWKRAAS 482
D 559 QDILDLTEDNR-----EWYQSTIP-QSPSPAD-----DPEEGROGOTEKQF 600
QY 483 GITNOMSIDELSPCEEAAPPSPAD 507
D 601 ELT--LEEDGESDTEKDSGQVEED 623

RESULT 14
US-10-067-514-8
; Sequence 8, Application US/10067514
; Publication No. US20030054531A1
; GENERAL INFORMATION:
; APPLICANT: Gretaasdotir, Solveig
; APPLICANT: Jonsdottir, Sif
; APPLICANT: Reynisdottir, Sigridur Th.
; TITLE OF INVENTION: HUMAN STROKE GENE
; FILE REFERENCE: 2345.2010-003
; CURRENT FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: US 09/811/352
; PRIOR FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 673
; TYPE: PRT
; ORGANISM: Human
US-10-067-514-8

Query Match
Best Local Similarity 23.1%; Score 617.5; DB 15; Length 687;
Matches 151; Conservative 105; Mismatches 174; Indels 75; Gaps 14;

QY 24 KOLENGEI-NIEELKKLEYTASLLLEAVYIDETROILDTDELEQLRSDAVPSEVDWLA 82
D 187 KRLNRELTHLSEMSRSGNOVSEFISNTFLDKQHEV-----EIPSP-----227
QY 83 STFTQARAKGR-AEEKPKFRSIVHVAQAGIFVERMFRRTYTSVGTYST-----AVL 135
D 228 ---TOKEKEKKRPMQISGVKKLMHSSSL-----TNSSI-PRFGVKTEQEDVLA 273
QY 136 NCLKNLDLWCFDVFSLNQADDAHALRTIVFELLTRNLNLSRFPKIPVFLMSFLDALETGY 195
D 274 KELEDVKNKGLHVFRIAELSGNRPLVIMHTIFQERDLTKFKIPVDTLITYLMTLEDHY 333
QY 196 GYKKNPYHNOIHAADVTQTVHCFLLRTGMVHCLSEIELLAIIPAAAIHDEYHTGTNSFH 255
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Db 334 -HADVAYHNNIHAADVQSTHLLSTPALEAVFTDLEILAAIFASAIHDVDHPGVSNQFL 392
QY 256 IOTKSECAIVYNDNRVLENNHSSVFRMLQDDMMIFNLTKDEFVELRALVIEVMTATD 315
Db 393 INTNSELALMYNDSSVLENNHLLAVGFKLLQEECDIFQNLTKKQSRKMYIDIVLATD 452
QY 316 MSCHFQOVKTKMTALQOLE-----RIDKPKALSLLHAADISHPTKQWLVSRSW 364
Db 453 MSKHNMLADLKTWVETKVTSSGVLILLDNTSDRIQVLMVHCADLSNPTKPLQLYRQW 512
QY 365 TKALMEEFROGDKAEGLCLPESPLCDRTSTLVAQSQIGFIDFIVEPTFSVLTDVAEKSV 424
Db 513 TDRIMEEFROGDRERERGMETSPMCDKHNASVEKSVQVGFIDYIVHPLWETWADLVHPDA 572
QY 425 QPLAD--EDSKSKNQPWFQWRQPSLDVEVGDNDPVDVSPRSTWVKRIQENKOKWKERAAS 482
Db 573 QDILTLEDNR-----EWQSTIP-QSPSPAPD-----DPEEGROGQTEKFQF 614
QY 483 GITNQMSIDELSPCEEAPPSPAPD 507
Db 615 ELT--LEEDGESDTEKDSGSQVEED 637

RESULT 15
US-10-076-597-50
; Sequence 50, Application US/10076597
; Publication No. US20030045490A1
; GENERAL INFORMATION:
; APPLICANT: Dale, Roderic M. K.
; APPLICANT: Arrow, Amy
; APPLICANT: Thompson, Terry
; TITLE OF INVENTION: Antisense Phosphodiesterase Inhibitors
; FILE REFERENCE: OLIG-003CIP
; CURRENT APPLICATION NUMBER: US/10/076,597
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/364,626
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/223,586
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 50
; LENGTH: 745
; TYPE: PRT
; ORGANISM: human
US-10-076-597-50

Query Match 23.1%; Score 617.5; DB 15; Length 745;
Best Local Similarity 29.9%; Pred. No. 5.6e-51;
Matches 151; Conservative 105; Mismatches 174; Indels 75; Gaps 14;
QY 24 KOLENGEI-NIEELKKNLEYTASLEAVYIDETQILDTEDLQELRSVAVPSEVRDMLA 82
Db 245 KRLNRELTHLSEMSRSGNQVSEFISNFTLDKQHEV-----EIPSP----- 285
QY 83 STFTQARAKGR-AFEKPKRSIVHAYQAGIFVERMERFRTYTSVGPYST-----AVL 135
Db 286 ----TQREKKRKPMSQISGVKRLMHSSSL-----TNSSI-PREGVKTQEDVLA 331
QY 136 NCLKNLDLWCFVFSINQAADHALRTIVFELLTRHNLISREKIPVFLMSFLDALETGY 195
Db 332 KELEDVKNKGLHVFRIAELSGNRPLTVIMHTIFQERDLKTKIPVDITLITVMTLEDHY 391
QY 196 GRYKNPNYHQAADVOTVCHVFLRTGMVHCLSEIELLAIIFAAAIHDHYEHTGTNSPH 255
Db 392 -HADVAYHNNIHAADVQSTHLLSTPALEAVFTDLEILAAIFASAIHDVDHPGVSNQFL 450
QY 256 IOTKSECAIVYNDNRVLENNHSSVFRMLQDDMMIFNLTKDEFVELRALVIEVMTATD 315
Db 451 INTNSELALMYNDSSVLENNHLLAVGFKLLQEECDIFQNLTKKQSRKMYIDIVLATD 510
QY 316 MSCHFQOVKTKMTALQOLE-----RIDKPKALSLLHAADISHPTKQWLVSRSW 364

Db 511 MSKHNMLADLKTWVETKVTSSGVLILLDNTSDRIQVLMVHCADLSNPTKPLQLYRQW 570
QY 365 TKALMEEFROGDKAEGLCLPESPLCDRTSTLVAQSQIGFIDFIVEPTFSVLTDVAEKSV 424
Db 571 TDRIMEEFROGDRERERGMETSPMCDKHNASVEKSVQVGFIDYIVHPLWETWADLVHPDA 630
QY 425 QPLAD--EDSKSKNQPWFQWRQPSLDVEVGDNDPVDVSPRSTWVKRIQENKOKWKERAAS 482
Db 631 QDILTLEDNR-----EWQSTIP-QSPSPAPD-----DPEEGROGQTEKFQF 672
QY 483 GITNQMSIDELSPCEEAPPSPAPD 507
Db 673 ELT--LEEDGESDTEKDSGSQVEED 695

Search completed: August 11, 2003, 01:25:35
Job time : 339 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 11, 2003, 00:55:06 ; Search time 44 seconds
(without alignments)
1127.796 Million cell updates/sec

Title: US-09-663-481-1

Perfect score: 2676

Sequence: 1 MANPVPVQSHLQPIRLR.....EEAPPSPAEDHNGNGLD 516

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616882 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_76:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2582	96.5	536	1 JC6129	3',5'-cyclic-nucle
2	2491	93.1	535	1 A44161	3',5'-cyclic-nucle
3	2489	93.0	535	1 A46378	3',5'-cyclic-nucle
4	2484.5	92.8	534	1 A44162	3',5'-cyclic-nucle
5	1610.5	60.2	519	2 T14783	hypothetical prote
6	1594	59.6	768	2 T10796	3',5'-cyclic-nucle
7	1591.5	59.5	530	1 A45334	3',5'-cyclic-nucle
8	1503	56.2	491	2 A40283	3',5'-cyclic-nucle
9	1254.5	46.9	664	2 T24459	hypothetical prote
10	638	23.8	549	2 T16769	hypothetical prote
11	626	23.4	712	2 S71626	3',5'-cyclic-nucle
12	622.5	23.3	844	2 I53865	phosphodiesterase
13	620	23.2	610	2 I67946	3',5'-cyclic-nucle
14	617.5	23.1	584	2 B53109	3',5'-cyclic-nucle
15	617.5	23.1	673	2 I61358	3',5'-cyclic-nucle
16	616	23.0	536	2 I67945	3',5'-cyclic-nucle
17	615	23.0	562	2 I59143	CAMP phosphodieste
18	613	22.9	786	2 I61354	phosphodiesterase
19	613	22.9	836	2 A54442	3',5'-cyclic-nucle
20	612.5	22.9	672	2 I61259	3',5'-cyclic-nucle
21	611	22.8	777	2 S65543	3',5'-cyclic-nucle
22	610.5	22.8	564	2 J61519	3',5'-cyclic-nucle
23	609.5	22.8	564	2 A40949	cyclic-AMP phospho
24	542	20.3	323	2 S5348	3',5'-cyclic-nucle
25	516	19.3	267	2 B33904	CAMP phosphodieste
26	511	19.1	1054	2 T30901	cyclic nucleotide
27	481.5	18.0	1112	2 S70522	cyclic nucleotide
28	481.5	18.0	1141	2 A44093	cGMP-inhibited CAM
29	478.5	17.9	1108	2 A48508	cyclic-nucleotide

RESULT 1

JC6129

3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 1B, calmodulin-dependent, 63k N:Alternate names: 63K calmodulin-stimulated phosphodiesterase, brain; CAM-PDE1B1 C:Species: Homo sapiens (man) C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 21-Jul-2000 C:Accession: JC6129; G02260 R:Jiang, X.; Li, J.; Faskind, M.; Epstein, P.M. Proc. Natl. Acad. Sci. U.S.A. 93, 11236-11241, 1996 A:Title: Inhibition of calmodulin-dependent phosphodiesterase induces apoptosis in hu A:Reference number: JC6129; MUID:97008163; PMID:8855339 A:Accession: JC6129 A:Molecule type: mRNA A:Residues: 1-536 <JIA> A:Cross-references: GB:U56976; NID:gl621591; PIDN:AAC50769.1; PID:gl621592 A:Experimental source: lymphoblastoid B-cell R:Houslay, M.D.; Erdogan, S.; Rena, G.; Sullivan, M. submitted to the EMBL Data Library, November 1995 A:Reference number: H00937 A:Accession: G02260 A:Status: translated from GB/EMBL/DBJ A:Molecule type: mRNA A:Residues: 201-203, 'W', 205-358, 'S', 360-384 <HOU> A:Cross-references: EMBL:040584; NID:gl110534; PID:gl110533 C:Comment: This enzyme is a useful target for inducing the death of leukemic cells. C:Genetics: A:Gene: GDB:PDE1B; PDES1B A:Cross-references: GDB:I20264; OMIM:171891 A:Map position: 16p13.11 C:Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3' C:Keywords: alternative splicing; calmodulin binding; cGMP binding; phosphoric dieste F:222-439/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNPD>

Query Match 96.5%; Score 2582; DB 1; Length 536;
Best Local Similarity 100.0%; Pred. No. 3.3e-184;
Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	19	LYRMVQLENGEINTEELKKNLEYTASLEAVYIDETROIILDEQLRSDAVSEVR	78
DB	39	LYRMVQLENGEINTEELKKNLEYTASLEAVYIDETROIILDEQLRSDAVSEVR	98
QY	79	DWLASTFTQQAARAKERRAEKPKFRSIVHVAOAGIFVERMFRRTVTSVGPTYSTAVLNCL	138
DB	99	DWLASTFTQQAARAKERRAEKPKFRSIVHVAOAGIFVERMFRRTVTSVGPTYSTAVLNCL	158
QY	139	KNLDLWCDFVSLNQADDDHALRTIVFELLTRHNLISRFKIPTVFLMSFLDALETGYGYK	198
DB	159	KNLDLWCDFVSLNQADDDHALRTIVFELLTRHNLISRFKIPTVFLMSFLDALETGYGYK	218
QY	199	KNPYHNOIHAADVTQTVHCFLRTGMVHCLSEIELLAIFAAAIHDYEHGTGTTNSFHQT	258
DB	219	KNPYHNOIHAADVTQTVHCFLRTGMVHCLSEIELLAIFAAAIHDYEHGTGTTNSFHQT	278

259 KSECAIYNDRSVLENHHISVFRMLQDDMMNIFINLTKEFVELRALVIEMLATDMSC 318
|||||
279 KSECAIYNDRSVLENHHISVFRMLQDDMMNIFINLTKEFVELRALVIEMLATDMSC 338
|||||
319 HFQOVKMTALQOOLERIDPKKALSLLHAADISHTPTKQWLVHSRWTKALMEEFFRQGD 378
|||||
339 HFQOVKMTALQOOLERIDPKKALSLLHAADISHTPTKQWLVHSRWTKALMEEFFRQGD 398
|||||
379 EAEGLPSPPLCDRTSTLVAQSIGFDIVETFSVLTQVAKSVQPLADESKSNQP 438
|||||
399 EAEGLPSPPLCDRTSTLVAQSIGFDIVETFSVLTQVAKSVQPLADESKSNQP 458
|||||
439 SFQWRQPSLDVEGDPNDVVSFRSTWVKIQENKQKWKRAASGTTNQMSIDELSPCEE 498
|||||
459 SFQWRQPSLDVEGDPNDVVSFRSTWVKIQENKQKWKRAASGTTNQMSIDELSPCEE 518
|||||
499 EAPPSPAEDHNGNGLD 516
519 EAPPSPAEDHNGNGLD 536
|||||
RESULT 2
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A:Accession: A44161
A:Molecule type: mRNA
A:Residues: 1-535 <REP>
A:Cross-references: GB:M94537; NID:g203268; PIDN:AAA16530.1; PID:g203269
A:Experimental source: brain
A:Note: sequence extracted from NCBI backbone (NCBIP:113357)
C:Comment: This enzyme is a useful target for inducing the death of leukemic cells, and
C:Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'
C:Keywords: alternative splicing; calmodulin binding; cGMP binding; phosphoric diester
F;221-438/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNPD>
Query Match 93.1%; Score 2491; DB 1; Length 535;
Best Local Similarity 95.8%; Pred. No. 2e-177;
Matches 477; Conservative 13; Mismatches 8; Indels 0; Gaps 0;
19 LRYMVKQLENGEINIEELKNLEYTASLLEAVYIDETQILDTDELOELRSDAVPSEVR 78
|||||
38 LRYMVKQLENGEINIEELKNLEYTASLLEAVYIDETQILDTDELOELRSDAVPSEVR 97
|||||
79 DWLASTFTQOARAKGRRAEKPFRSIVHAVQAGIFVERMFRRTYTSVGPTYSTAVLNCL 138
|||||
98 DWLASTFTQOARAKGRRAEKPFRSIVHAVQAGIFVERMFRRTYTSVGPTYSTAVLNCL 157
|||||
139 KNLDMCFDVSFNQAADHALRTIVFELLTRHNLISREKIPVFLMSFLDALETGYGY 198
|||||
158 KNLDMCFDVSFNQAADHALRTIVFELLTRHNLISREKIPVFLMSFLDALETGYGY 217
|||||
199 KNPYHNOIHAADVTQVHCFLRTGMVHCLSELELLAIFAAAIHDYHTGTTNSPHIQ 258
|||||
218 KNPYHNOIHAADVTQVHCFLRTGMVHCLSELELLAIFAAAIHDYHTGTTNSPHIQ 277
|||||
259 KSECAIYNDRSVLENHHISVFRMLQDDMMNIFINLTKEFVELRALVIEMLATDMSC 318
|||||
278 KSECAIYNDRSVLENHHISVFRMLQDDMMNIFINLTKEFVELRALVIEMLATDMSC 337
|||||
319 HFQOVKMTALQOOLERIDPKKALSLLHAADISHTPTKQWLVHSRWTKALMEEFFRQGD 378
|||||
338 HFQOVKMTALQOOLERIDPKKALSLLHAADISHTPTKQWLVHSRWTKALMEEFFRQGD 397
|||||

379 EAEGLPSPPLCDRTSTLVAQSIGFDIVETFSVLTQVAKSVQPLADESKSNQP 438
|||||
398 EAEGLPSPPLCDRTSTLVAQSIGFDIVETFSVLTQVAKSVQPLADESKSNQP 457
|||||
439 SFQWRQPSLDVEGDPNDVVSFRSTWVKIQENKQKWKRAASGTTNQMSIDELSPCEE 498
|||||
458 SFQWRQPSLDVEGDPNDVVSFRSTWVKIQENKQKWKRAASGTTNQMSIDELSPCEE 517
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499 EAPPSPAEDHNGNGLD 516
518 EAPPSPAEDHNGNGLD 535
|||||
RESULT 3
A46378
A:Accession: A46378
A:Molecule type: mRNA
A:Residues: 1-535 <POL>
A:Cross-references: GB:I01695; NID:g200269; PIDN:AAA39902.1; PID:g200270
A:Experimental source: brain
A:Note: sequence extracted from NCBI backbone (NCBIP:113365)
C:Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3'
C:Keywords: alternative splicing; calmodulin binding; cGMP binding; phosphoric diester
F;221-438/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>
Query Match 93.0%; Score 2489; DB 1; Length 535;
Best Local Similarity 95.8%; Pred. No. 2.8e-177;
Matches 477; Conservative 12; Mismatches 9; Indels 0; Gaps 0;
19 LRYMVKQLENGEINIEELKNLEYTASLLEAVYIDETQILDTDELOELRSDAVPSEVR 78
|||||
38 LRYMVKQLENGEINIEELKNLEYTASLLEAVYIDETQILDTDELOELRSDAVPSEVR 97
|||||
79 DWLASTFTQOARAKGRRAEKPFRSIVHAVQAGIFVERMFRRTYTSVGPTYSTAVLNCL 138
|||||
98 DWLASTFTQOARAKGRRAEKPFRSIVHAVQAGIFVERMFRRTYTSVGPTYSTAVLNCL 157
|||||
139 KNLDMCFDVSFNQAADHALRTIVFELLTRHNLISREKIPVFLMSFLDALETGYGY 198
|||||
158 KNLDMCFDVSFNQAADHALRTIVFELLTRHNLISREKIPVFLMSFLDALETGYGY 217
|||||
199 KNPYHNOIHAADVTQVHCFLRTGMVHCLSELELLAIFAAAIHDYHTGTTNSPHIQ 258
|||||
218 KNPYHNOIHAADVTQVHCFLRTGMVHCLSELELLAIFAAAIHDYHTGTTNSPHIQ 277
|||||
259 KSECAIYNDRSVLENHHISVFRMLQDDMMNIFINLTKEFVELRALVIEMLATDMSC 318
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278 KSECAIYNDRSVLENHHISVFRMLQDDMMNIFINLTKEFVELRALVIEMLATDMSC 337
|||||
319 HFQOVKMTALQOOLERIDPKKALSLLHAADISHTPTKQWLVHSRWTKALMEEFFRQGD 378
|||||
338 HFQOVKMTALQOOLERIDPKKALSLLHAADISHTPTKQWLVHSRWTKALMEEFFRQGD 397
|||||
379 EAEGLPSPPLCDRTSTLVAQSIGFDIVETFSVLTQVAKSVQPLADESKSNQP 438
|||||

398	Db	EAEGLPSPCLDRTSLVAQSQIGTFDIVEPTFSLTVDAEKSYQLADDDSKPKSQP	457
439	QY	SFQWRQPSLDYVEVGDPNPDVVSFRSTWVKIQENKQWKERAASGTINOMSIDELSPCEE	498
458	Db	SFQWRQPSLDYVDGDPNDPVVSFRATWTKIQENKQWKERAASGTINOMSIDELSPCEE	517
499	QY	EAPSPSPAEDEHNQNGNLD	516
518	Db	EAPSPSPAEDEHNQNGNLD	535

RESULT 4
A44162
3', 5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 1B, calmodulin-dependent, 63K sp
N; Alternate names: 63K calmodulin-stimulated phosphodiesterase, brain; CAM-PDE1B1
C; Species: Bos primigenius taurus (cattle)
C; Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 05-Nov-1999
C; Accession: A44162; B40283
R; Bentreley, J.K.; Kadlecsek, A.; Sherbert, C.H.; Seger, D.; Sonnenburg, W.K.; Charbonneau,
J. J. Biol. Chem. 267, 18676-18682, 1992
A; Title: Molecular cloning of cDNA encoding a "63"-kDa calmodulin-stimulated phosphodies
A; Reference number: A44162; MUID:92406781; PMID:1326531

Qy	439	SFQWRQPSLDVEVGDPNDVVYFSRSTWWKRTQENKQKWKRAAASGITNOMSIDELSPCEE	498
Db	457	SFQWRQPSLDVEVGDPNDVVYFSRSTWTKYIQENKQKWKRAAASGITNOMSIDELSPCEE	516
Qy	499	EAPSPAEDEHNQNGNLD	516
Db	517	EAPASPAEDEHNQNGNLD	534

RESULT 5

T14783
hypothetical protein DKFzp586G0221.1 - human
C:Species: Homo sapiens (man)
C:Date: 20-Sep-1999 #sequence_revision' 20-Sep-1999 #text
C:Accession: T14783
R:Ottewaelder, B.; Obermaier, B.; Meves, H.W.; Gassenhuh
submitted to the Protein Sequence Database, August 1999
A:Reference number: Z18184
A:Accession: T14783
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-519 <OTT>
A:Cross-references: EMBL:AL110263
A:Experimental source: adult uterus; clone DKFzp586G0221.1
C:Genetics:
A:Note: DKFzp586G0221.1
C:Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase
F:202-419/Domain: 3',5'-cyclic-nucleotide phosphodiester

RESULT 6
T10796

3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 02-Sep-2000
C:Accession: T10796
R:Yan, C.; Zhao, A.Z.; Bentley, J.K.; Loughney, K.; Ferguson, K.; Beavo, J.A.
Proc. Natl. Acad. Sci. U.S.A. 92, 9677-9681, 1995
A:Title: Molecular cloning and characterization of a calmodulin-dependent phosphodiesterase
A:Reference number: 217151; MUID:96003842; PMID:7568196
A:Accession: T10796
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-768 <YAN>
A:Cross-references: EMBL:L41045; MID:9871804; PIDN:AB00868.1; PID:9871805
A:Experimental source: strain Norway, Olfactory mucosa
C:Genetics:
C:Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase homology
C:Keywords: phosphoric diester hydrolase
F:287-505/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>
Query Match 59.6%; Score 1594; DB 2; Length 768;
Best Local Similarity 60.5%; Pred. No. 1.7e-110;
Matches 310; Conservative 81; Mismatches 81; Indels 40; Gaps 5;
QY 18 RLRYMVKQLNGEINTIEELKKNLEYTASLEAVYIDETROILDTDELOELSDAVPSEV 77
Db 103 RLRLVVKQLNGEINTIEELKKNLEYTASLEAVYIDETROILDTDELOELSDAVPSEV 162
QY 78 RDLMASTFTQOARAKGRRAEKPFRSIVHAGVAGIFVERMFRRTYTSVGTPTSTAVLNC 137
Db 163 RDLMASTFTQOARAKGRRAEKPFRSIVHAGVAGIFVERMFRRTYTSVGTPTSTAVLNC 222
QY 138 LKNDLWCDFVSLNQAADHALRTIVFELLTRNLISRPKIPVFLMSFLDALEGTGK 197
Db 223 LKNDVTSDFVSLNQAADHALRTIVFELLTRNLISRPKIPVFLMSFLDALEGTGK 282
QY 198 YKPYHNOIHAADVDTQVHCFLLRTGMVHCLSEIELLAIIFAAAHYDHTGTNSPHIQ 257
Db 283 HKNPYHNLMAADVDTQVHCFLLRTGMVHCLSEIELLAIIFAAAHYDHTGTNSPHIQ 342
QY 258 TKSECATVYNDRSVLENNHSSVFLRMQDDEENIFNLTKDFVELRALVEMVLATDM 316
Db 343 TRSDPALLYNDRSVLENNHSSVFLRMQDDEENIFNLTKDFVELRALVEMVLATDM 402
QY 317 SCHFOQVKMTALQOLERIDKPKALSLHLLHAADISHPTKQWLHVSRTKALMEEFRRQ 376
Db 403 SCHFOQVKMTALQOLERIDKPKALSLHLLHAADISHPTKQWLHVSRTKALMEEFRRQ 452
QY 377 DKAEGLPSPICDRFTSTLVAQSQIGFIDFIVEPTFSTVLTDAEKSQVPLADESKSN 436
Db 463 DKAEGLPSPICDRFTSTLVAQSQIGFIDFIVEPTFSTVLTDAEKSQVPLADESKSN 522
QY 437 QPSFQWRQPSLD-VEVGDPN-----PDVVSFRSTWVKRIQENKQ 474
Db 523 TQO---RRSLNSINSDDAKRSQVSGSGSAPINNSVIPVDYKSKFATWTEVQINRE 579
QY 475 KWKERAASGITNOMSIDELSPCEEAPPSPAE 506
Db 580 RWRKRV-----PKEEKAKKEAE 597

RESULT 7
A45334
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 1A, calmodulin-dependent, 61k bp
N:Alternate names: 61K cyclic-nucleotide phosphodiesterase, brain
C:Species: Bos primigenius taurus (cattle)
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 05-Nov-1999
C:Accession: A45334; A40282; A26650; A54958
R:Sonnenburg, W.K.; Seger, D.; Beavo, J.A.
J. Biol. Chem. 268, 645-652, 1993
A:Title: Molecular cloning of a cDNA encoding the "61-kDa" calmodulin-stimulated cyclic
A:Reference number: A45334; MUID:93107074; PMID:7678006
A:Accession: A45334

A:Molecule type: mRNA
A:Residues: 1-530 <SON>
A:Cross-references: GB:M90358; MID:g162878; PIDN:AAA74560.1; PID:g162879
A:Experimental source: brain
R:Charbonneau, H.; Kumar, S.; Novack, J.P.; Blumenthal, D.K.; Griffin, P.R.; Shabanow
Biochemistry 10, 7931-7940, 1991
A:Title: Evidence for domain organization within the 61-kDa calmodulin-dependent cyclic
A:Reference number: A40282; MUID:91329365; PMID:1651111
A:Accession: A40282
A:Molecule type: protein
A:Residues: 1-530 <CHA>
A:Experimental source: brain
R:Charbonneau, H.; Beier, N.; Walsh, K.A.; Beavo, J.A.
Proc. Natl. Acad. Sci. U.S.A. 83, 9308-9312, 1986
A:Title: Identification of a conserved domain among cyclic nucleotide phosphodiesterase
A:Reference number: A26650; MUID:87092242; PMID:3025833
A:Accession: A26650
A:Molecule type: protein
A:Residues: 194-211, 'X', 213-236, 'G', 238-273, 'X', 275-320, 'W', 322-374, 'XKL', 378-427 <CH>
R:Florio, V.A.; Sonnenburg, W.K.; Johnson, R.; Kwak, K.S.; Jensen, G.S.; Walsh, K.A.;
Biochemistry 13, 8948-8954, 1994
A:Title: Phosphorylation of the 61-kDa calmodulin-stimulated cyclic nucleotide phosph
A:Reference number: A54958; MUID:94318639; PMID:8043581
A:Accession: A54958
A:Status: preliminary
A:Molecule type: protein
A:Residues: 105-109; 116-125; 138-142; 156-160; 453, 'X', 455-460; 503-505, 'X', 507-512 <FLO>
C:Complex: homodimer
C:Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3'
F:2-530/Product: 3',5'-cyclic-nucleotide phosphodiesterase 1A, calmodulin-dependent;
F:24-42/Region: calmodulin binding
F:218-435/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>
F:2/Modified site: acetylated amino end (Gly) (in mature form) status experimental
F:120,138/Binding site: phosphate (Ser) (covalent) (by protein kinase A) status exper
Query Match 59.5%; Score 1591.5; DB 1; Length 530;
Best Local Similarity 61.2%; Pred. No. 1.6e-110;
Matches 300; Conservative 91; Mismatches 90; Indels 9; Gaps 1;
QY 19 LRYMVKQLNGEINTIEELKKNLEYTASLEAVYIDETROILDTDELOELSDAVPSEVR 78
Db 35 LRCLVVKQLNGEINTIEELKKNLEYTASLEAVYIDETROILDTDELOELSDAVPSEVR 94
QY 79 DWLASTFTQOARAKGRRAEKPFRSIVHAGVAGIFVERMFRRTYTSVGTPTSTAVLNC 138
Db 95 DWLASTFTQOARAKGRRAEKPFRSIVHAGVAGIFVERMFRRTYTSVGTPTSTAVLNC 154
QY 139 LKNDLWCDFVSLNQAADHALRTIVFELLTRNLISRPKIPVFLMSFLDALEGTGKY 198
Db 155 KDVKWSEDFVSLNQAADHALRTIVFELLTRNLISRPKIPVFLMSFLDALEGTGKY 214
QY 199 KNPYHNOIHAADVDTQVHCFLLRTGMVHCLSEIELLAIIFAAAHYDHTGTNSPHIQ 258
Db 215 KNPYHNLMAADVDTQVHCFLLRTGMVHCLSEIELLAIIFAAAHYDHTGTNSPHIQ 274
QY 259 KSECATVYNDRSVLENNHSSVFLRMQDDEENIFNLTKDFVELRALVEMVLATDMSC 318
Db 275 RSDVALLYNDRSVLENNHSSVFLRMQDDEENIFNLTKDFVELRALVEMVLATDMSC 334
QY 319 HFOQVKMTALQOLERIDKPKALSLHLLHAADISHPTKQWLHVSRTKALMEEFRRQDK 378
Db 335 HFOQVKMTALQOLERIDKPKALSLHLLHAADISHPTKQWLHVSRTKALMEEFRRQDK 394
QY 379 EAEGLPSPICDRFTSTLVAQSQIGFIDFIVEPTFSTVLTDAEKSQVPLADESKSNQ 438
Db 395 EAEGLPSPICDRFTSTLVAQSQIGFIDFIVEPTFSTVLTDAEKSQVPLADESKSNQ 454
QY 439 SFQWRQPSLDVEVGDPN-----PNPDVVSFRSTWVKRIQENKQKRAASGITNOMS 489
Db 455 YGASRRSRNMKGTTNDGTYSPTYSLASVDLKSFKNSLVLDIIQQNKWKELAAQGEPPPHK 514

QY 490 IDELSPEEE 499
Db 515 NSDLVNAEK 524

RESULT 8
A40283
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17), calmodulin-dependent, 59K card
C:Species: Bos primigenius taurus (cattle)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 21-Jan-2000
C:Accession: A40283
R:Novack, J.P.; Charbonneau, H.; Bentley, J.K.; Walsh, K.A.; Beavo, J.A.
Biochemistry 30, 7940-7947, 1991
A:Title: Sequence comparison of the 63-, 61-, and 59-kDa calmodulin-dependent cyclic nu
A:Reference number: A40283; MUID:91329366; PMID:1651112
A:Accession: A40283
A:Molecule type: protein
A:Residues: 1-491 <NOV>
C:Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'
C:Keywords: calmodulin binding; cardiac muscle; heart; phosphoric diester hydrolase
F:196-396/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CN>

Query Match 56.2%; Score 1503; DB 2; Length 491;
Best Local Similarity 57.9%; Pred. No. 5.4e-104;
Matches 294; Conservative 90; Mismatches 92; Indels 32; Gaps 6;

QY 1 MANPVVORSHLGGPTLRLRYMVKOLENGEINIEELKNLEYTASLLEAVYIDETRIQILD 60
Db 1 MDDHTIRKHLQRIPLRLCLVQLKQEGDGNVLDLKNIEYAASVLEAVYIDETRIQLD 60

QY 61 TEDELQELSDAVPSEVRDLASTTQQARAKGRRAEKPFRSIVHVAQAGIFVERMPR 120
Db 61 TDELSDIQSDVPSEVRDLASTFMK-----KKSEKPRFRSIVHVVQAGIFVERMYR 115

QY 121 RYTSVGPITYSTAVLNCLNLDLWCFDVFSLNQADDDHALRTIVPELTLRHNLISRFKIP 180
Db 116 KSYHVMGLAYPEAVITLKDVKDFVFNALNEASGEHSLK-MIYELETRYDLINRFKIP 174

QY 181 TVFLMSFLDALGTGKYKNPYHNOIHAADVTQTVHCFLLRTGMVHCLSEIELLALIFAA 240
Db 175 VSLCLAFPAEALGVGSKYKNPYHNLIIHAADVTQTVHYIMLTGIMHNLTELEILLAMVFAA 234

QY 241 AIHDYEHTGTTNSFHIOKSECAIYVNDRSVLNHHISSVFRMLQDDENINILTKDEF 300
Db 235 AIHDYEHTGTTNHFHIOKSECAIYVNDRSVLNHHISSVFRMLQDDENINILTKDEF 288

QY 301 VELRALVIVMLATDMSCHFQOVKMTALQOLERIDPKALSLLHAAIDSHPTKQWLIV 360
Db 289 RDLRLNVLVIEL-----STKNIRNSLQOPEGLDK-KTMSLILHAAIDSHPAKSWKL 337

QY 361 HSRWTKALMEEPFROGDKAEALGLPFLPCDRSTLTVAQSQIGFIDFIVEPTFSVLTDA 420
Db 338 HHRWTMALMEEPFROGDKAEALGLPFLPCDRKRTVAQSQIGFIDFIVEPTFSVLTST 397

QY 421 EKSVOPLADEDSKSNQPSFQWRQPSLDVEVDG-----PNPDVVSFRSTWTKRIOE 471
Db 398 EKIIITLIEEDSKTTPSYGASRSRMKGTNDGYSPDYSLASVDLAKSFKNLSLVDITQQ 457

QY 472 NKQWKERAAAGITNQMIDELSPCEE 499
Db 458 NKERWELAAQGEPPHKNNSDLVNAEK 485

RESULT 9
T24459
hypothetical protein T04D3.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000
C:Accession: T24459
R:Kershaw, J.
submitted to the EMBL Data Library, October 1996
A:Reference number: 219893

A:Accession: T24459
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-664 <WIL>
A:Cross-references: EMBL:281114; PIDN:CAB03289.1; GSPDB:GN00019; CESP:T04D3.3
A:Experimental source: clone T04D3
C:Genetics:
A:Gene: CESP:T04D3.3
A:Map position: 1
A:Introns: 52/3; 102/1; 152/2; 190/2; 355/3; 465/2; 553/3; 589/2; 634/1; 660/1
C:Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase homology
F:332-549/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CN>

Query Match 46.9%; Score 1254.5; DB 2; Length 664;
Best Local Similarity 47.0%; Pred. No. 2.5e-85;
Matches 255; Conservative 92; Mismatches 139; Indels 57; Gaps 11;

QY 8 QRSHLQGPIL----RLRYMVKOLENGEINIEELKNLEYTASLLEAVYIDETRIQILD 63
Db 138 KKSNDNAPALESLEKLYILHQLNSQLPLEDLKRNIEYAALVLETAYWDETTRICDEDD 197

QY 64 ELQELSDAVPSEVRDLASTTQQARAKGRRAEKPFRSIVHVAQAGIFVERMPR 123
Db 198 DLAEVTPETVPDEVRDLASTTQQARAKGRRAEKPFRSIVHVAQAGIFVERMPR 254

QY 124 TSVGPTYSTAVLNCLNLDLWCFDVFSLNQADDDHALRTIVPELTLRHNLISRFKIP 183
Db 255 VVQCP-IPPEIAELMKEVCTWSFSPQLNEVSEGHALKYVGFELFNRYGFMORFKVPLTA 313

QY 184 LMSFLDALGTGKYKNPYHNOIHAADVTQTVHCFLLRTGMVHCLSEIELLALIFAA 243
Db 314 LENYLSALEVGVGSKYKNPYHNVVHAADVTQSSHFMSLQGLANSGLDELLAVLFGALIH 373

QY 244 DYEHGTGTTNSFHIOKSECAIYVNDRSVLNHHISSVFRMLQDDENINILTKDEF 303
Db 374 DYEHGTGTTNHFHIOKSECAIYVNDRSVLNHHISSVFRMLQDDENINILTKDEF 433

QY 304 RALVIVMLATDMSCHFQOVKMTALQOLERIDPKALSLLHAAIDSHPTKQWLIV 363
Db 434 RNMVIEIVLATDMSCHFQOVKMTALQOLERIDPKALSLLHAAIDSHPTKQWLIV 493

QY 364 WTKALMEEPFROGDKAEALGLPFLPCDRSTLTVAQSQIGFIDFIVEPTFSVLTDA 423
Db 494 WTEGVLEEFROGDKAEALGLPFLPCDRSTLTVAQSQIGFIDFIVEPTFSVLTDA 553

QY 424 VQPL-----ADEDS-----KSKNQPSFQWRQ-----SLDVE 450
Db 554 VEPLVSLPPTDSLFPSPVSDGDDKSPSNALSPDLRNSSTSPSSIRRIPLNYAGKLDI- 612

QY 451 VGDPNPDPVVSFRSTWTKRIOENKQWKRAAAGITNQMIDELSPCEEAPPSPADEHN 510
Db 613 ---PTP-----WMKFLHKNKAHKKRAAKE-EERKIKEAA--EAEAAKQVE-ENK 657

QY 511 QNG 513
Db 658 ENG 660

RESULT 10
T16769
hypothetical protein R153.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jun-2000
C:Accession: T16769
R:Kirsten, J.
submitted to the EMBL Data Library, June 1995
A:Reference number: The sequence of C. elegans cosmid R153.
A:Reference number: Z18573
A:Accession: T16769
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-549 <KIR>
A:Cross-references: EMBL:U28729; NID:g861238; PID:g861239; PIDN:AAA68292.1; CESP:R153

A;Experimental source: strain Bristol N2

C;Genetics:

A;Gene: CESP:R153.1

A;Introns: 25/2; 56/3; 91/1; 116/3; 163/3; 304/3; 338/1; 389/3; 430/3; 491/3

C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'-

F;281-509/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <NCP>

Query Match 23.8%; Score 638; DB 2; Length 549;

Best Local Similarity 32.8%; Pred. No. 1.4e-39;

Matches 150; Conservative 89; Mismatches 157; Indels 62; Gaps 12;

24 KOLENGI-NIEELKKNLEYTASLEAVYIDETQRIIDTEDELQELSDAVPSVRDMLA 82

118 KMLNKLSHFAESSKSTQSKFLITTYNDKEDEPSIELE-----VPIEV----- 164

83 STFTQARAKGRRAEKPFRSIVHVAQAGIF-----VERMFRYTSVGTFTSTAVLNC 137

165 ---QGFSTSG-----PMTLSILKKAQTAAMNKISGVRLKRAPSHDGHVPEVG---VNC 211

138 -----LKNLDLWCFDPVPSLNOAADDHALRTIVFELLTRHNLISRKIPTVFLMSPLDA 190

212 ARETAVHQRDDGPDVFKIDELSKNHSITVTFSLRQNLKFTFEIHQSTLTVTLLN 271

191 LEFGYKYNPNQIHAADVTQVHCFLRTGMVHCLSELELAIFAAAIHDYHGT 250

272 LEHHY--RNHYHNFHAADVAOSMHVLLMSPVTEVFTDLEVLAAIFAGAVHDVHPGF 329

251 TNSPHIOTKSECAIVYNDNRVLENHHISVFRMLQDDMMNIFNLTKDEFVELRALVIEM 310

330 TNOYLINSNELAIMYNDSEVLQHLAVAFKLQDSNCDPLANLSRKORLOPKRIVIM 389

311 VLATDMSCHFOQVTKMTALQQ-----LERI-DKPKALSLLHAAADISHPKQWL 359

390 VLATDMSKMSLLADLTKVYEAKKVAGNNVILVDKYNKTLQVLSMTHLADLSNPKPIE 449

360 VHSRWTKALMEFFROGDKAEALGLPSPCLDRTSTLVAQSGIFDIFIVEPTFVLTVD 419

450 LYQOWNRIMEEYWRQDKELGLSEIPMCDRGNTIEKSGVGFIDYIYHPLYETWADL 509

420 AEKSVQPLADESKSNQPSFQWRQPSLDVEGDPNPD 457

510 VYDPAQNILDOLENR-----EWVQSRIPE-----PD 537

RESULT 11

S71626

3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17), CAMP-specific - human

N;Alternate names: 3',5'-cyclic AMP phosphodiesterase

C;Species: Homo sapiens (man)

C;Date: 27-Nov-1997; #sequence_revision 12-Dec-1997 #text_change 17-Nov-2000

C;Accession: S71626, I61356

R;Engels, P.; Sullivan, M.; Mueller, T.; Luebbert, H.

FEB; Lett. 359, 305-310, 1995

A;Title: Molecular cloning and functional expression in yeast of a human cAMP-specific P

A;Reference number: S71626; MUID:95145731; PMID:7843419

A;Accession: S71626

A;Molecule type: DNA

A;Residues: 1-712 <ENG>

A;Cross-references: EMBL:246632; NID:g727222; PIDN:CAA86601.1; PID:g727223

A;Experimental source: substantia nigra

R;Bolger, G.; Michaeli, T.; Martins, T.; St. John, T.; Steiner, B.; Rodgers, L.; Riggs,

Mol. Cell. Biol. 13, 6558-6571, 1993

A;Title: A family of human phosphodiesterases homologous to the dunce learning and mem

A;Reference number: A54442; MUID:94019330; PMID:8413254

A;Accession: I61356

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 462-712 <RES>

A;Cross-references: GB:L20968; NID:g347125; PIDN:AAA03591.1; PID:g347126

C;Genetics:

A;Gene: HSPDB4C1

C;Function:

A;Description: cAMP hydrolysis; converts cAMP to non-cyclic AMP

A;Pathway: cyclic nucleotide metabolism

A;Note: expressed in various tissues but not in cells of the immune system

C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent;

C;Keywords: phosphoric diester hydrolase

F;367-615/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <NCP>

Query Match 23.4%; Score 626; DB 2; Length 712;

Best Local Similarity 29.2%; Pred. No. 1.6e-38;

Matches 151; Conservative 108; Mismatches 205; Indels 54; Gaps 12;

7 VORSHLOGLRLRYMVKOLENGEI-NIEELKNLEYTASLEAVYIDETQRIIDTEDEL 65

223 LOPHSVGMASKNKF--KRILNRELTHLSRSGNQSVSEYISRTFIDQ-----QTEVEL 275

66 QELRSDAVPSEVRDMLASTTQOARAKGRRAEKPFRSIVHVAQAGIFVERMPFRYTS 125

276 PKVTAEPAPDM-----SRISG-----LHGLCHSASLSATVPRE-----G 311

126 VGPTYTAVLNCNLKNDLWCFDPVPSLNOAADDHALRTIVFELLTRHNLISRKIPTVFLM 185

312 VQTDQEQALAKELEDTNKGLDVFKVADVSGNRPLTAIIFSIQERDLTKFTQIPADTLA 371

186 SPLDALETGYGKYNPNQIHAADVTQVHCFLRTGMVHCLSELELAIFAAAIHDY 245

372 TYLLMLE-GHYHANVAVHNSLHAADVAQSTHVLATPALEAVFTDLELAALFASAIHDV 430

246 EHTGTTNSPHIOTKSECAIVYNDNRVLENHHISVFRMLQDDMMNIFNLTKDEFVELRA 305

431 DHPGVSNQOFLINTNSDALMYNDASVLENHHLAVGFKLQAENCDFONLSAKORLSLR 490

306 LVTEMLVATDMSCHFQVTKMTALQOLE-----RIDKPKALSLLHAAADISHP 354

491 MVIDMVLATDMSKHMNLADLTKMTVETKVTSLGVLLLDNYSDRIQVLQNLVHCADLSNP 550

355 TKOWLVSRTWKALMEFFROGDKAEALGLPSPCLDRTSTLVAQSGIIGTDFIVERTES 414

551 TKPLPLYRQWTDRIAMAEFFQGDRESGLDISPMCDKHSTAEKVSQGVGIDYIAHPLWE 610

415 VLTDVAEKSVOPLAD--EDSKSNQPSFQWRQPSLDVEGDP---NPDVVYSERSTWVKRI 469

611 TWADLVHPDAQDLDTLED---NREWYQSKIPRPSDLTNPRDGDPRQFQFELTLEAE 666

470 OENKOKWKPRASAGITNO-MSIDELSPCEEEAPSPAE 506

567 EDEEEEEEGETALAKEALELPTTELLSPEAGDPDGD 704

RESULT 12

I53865

Phosphodiesterase - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 02-Sep-2000

C;Accession: I53865

R;Bolger, G.B.; Rodgers, L.K.; Riggs, M.

Gene 149, 237-244, 1994

A;Title: Differential CNS expression of alternative mRNA isoforms of the mammalian c

A;Reference number: I53865; MUID:95047482; PMID:7958996

A;Accession: I53865

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-844 <RES>

A;Cross-references: GB:L27057; NID:g3334904; PIDN:AAC27098.1; PID:g436004

C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase homology

F;418-646/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <NCP>

Query Match 23.3%; Score 622.5; DB 2; Length 844;

Best Local Similarity 30.6%; Pred. No. 3.7e-38;

Matches 161; Conservative 99; Mismatches 185; Indels 85; Gaps 16;

4 PVPV-ORSHLOGP-----ILRLRYMVKOLEN-----GEINIEE 35

197 PIPSNKRSLPGPPSVCKATLSETCQQLARETLEEDLWCLQELQETMQRYSRVSSEMASHK 256

QY 36 LKKNLEYTASLLEAV-----YIDETRIQILDTEDELQELRSDAVPSEVRDLASTFTT 86
Db 257 FRMLNRELTHLSEMSRSGNVEYSINT--FLDKQNEVE-----IPSTPRQRA--FQ 306
QY 87 QOARAKGRAEKP---FRSIVHAVQAGIFVERMFRRTYSVGTPTSTAVLNCLKNLDL 143
Db 307 QPPSVLQSQPMQMSQITGLKKLVHTGSLNTNVPRE-----GVKTDQEDLLAQELELSK 360
QY 144 MCFDVSFNQAADHALRTIIVFELLTRHNLISRFKIPTVFLMSFLDALETGYGKYNPYH 203
Db 361 WGLNIFCVSEYAGGRSLSCIMYTFQERDLLKKFHPVDVMMYMLTLEDHY-HADVAYH 419
QY 204 NOIHAADVTQTVHCELLRTGMVHCLSEIELLAIIFAAAIHDEYHTGTTNSFHQTKSECA 263
Db 420 NSLHAADVLQSTHVLATPALDAVFTDLEILAAALFAAAIHVDHDPGVSNQFLINTNSLA 479
QY 264 IYVNDRSVLENHHISSVFLRMQDDDMNIFINTKDEFVELRALVTEMVLATDMSCHFQV 323
Db 480 LMYNDESVLNHHLAGVFKLLQEECDIFQNLKQROSLRKQKMWIDMVLATDMSKHMILL 539
QY 324 KTMKTALQOLE-----RIDPKALSLLLHAADISHPTKQWLHVSRTWKALMEEF 372
Db 540 ADLKTMTVETKVTSSGVLLLDNYSDRIOVLNMVHCADLSNPTKPLELYRQWTDRIAEF 599
QY 373 FRQDKAEALGLPSPCLDRSTLVAQSOIGFIDFIVEPTFSVLTDVAEKSVQPLAD--E 430
Db 600 FQGDREERERGMETSPMDKHTASVEKSVQGFIDYIVHPLWETWADLVHPDAQDILDTLE 659
QY 431 DSKS-----KNQPSFQWRQPSLDVE---VGDPN-PDVVSFRSTVWVKRIQEN 472
Db 660 DNRDWHSAIROSPS-----PPEEPPGLGHPSLPDKFQFELTLEEEED 706
RESULT 13
I67946
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 4A, splice form 1 - rat
N:Alternate names: cyclic AMP-specific phosphodiesterase RD1; RNPDE4A1
N:Contains: 3',5'-cyclic-nucleotide phosphodiesterase 4A, splice form 2 (cyclic AMP-spec
hosphodiesterase RD3)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 29-May-1998 #sequence revision 29-May-1998 #text_change 24-Aug-2001
C:Accession: I67946; A32558; B32558; C32558
R:Bolger, G.B.; Rodgers, L.K.; Riggs, M.
Gene 149, 237-244, 1994
A:Title: Differential CNS expression of alternative mRNA isoforms of the mammalian genes
A:Reference number: I53865; MUID:95047482; PMID:7958996
A:Accession: I67946
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-610 <RES>
A:Cross-references: GB:L27062; NID:9436013; PIDN:AAA56859.1; PID:9436014
R:Davis, R.L.; Takayasu, H.; Eberwine, M.; Myres, J.
Proc. Natl. Acad. Sci. U.S.A. 86, 3604-3608, 1989
A:Title: Cloning and characterization of mammalian homologs of the Drosophila dunce(+) g
A:Reference number: A32558; MUID:89264472; PMID:2542942
A:Accession: A32558
A:Molecule type: mRNA
A:Residues: 1-598, 'T', 600-610 <DAV>
A:Cross-references: GB:M26715; NID:g203982; PIDN:AAC37699.1; PID:g203983; GB:J04554
A:Accession: B32558
A:Molecule type: mRNA
A:Residues: 85-120,154-598, 'T', 600-610 <DA2>
A:Cross-references: GB:M26716; GB:J04554; NID:g203986; PIDN:AAA41102.1; PID:g
A:Note: splice form RD2
A:Accession: C32558
A:Molecule type: mRNA
A:Residues: 26-598, 'T', 600-610 <DA3>
A:Cross-references: GB:M26716; NID:g203984; PIDN:AAA41101.1; PID:g203985; GB:J04554
A:Note: splice form RD3
C:Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'
Keywords: alternative splicing; cAMP binding; phosphoric diester hydrolase
F:14-20/Region: responsible for membrane association
F:26-610/Product: 3',5'-cyclic-nucleotide phosphodiesterase 4A, splice form 3 #status pr

F:85-120,154-610/Product: 3',5'-cyclic-nucleotide phosphodiesterase 4A, splice form 2
F:184-412/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>
Query Match 23.2%; Score 620; DB 2: Length 610;
Best Local Similarity 31.5%; Pred. No. 3.6e-38;
Matches 147; Conservative 96; Mismatches 163; Indels 60; Gaps 12;
QY 53 DETROIILTE-DELOELRSDAVPSEVRDLASTFTTQQ-----ARAKGRRAEKP--- 101
Db 21 DQFKRMLNRELTHLSEMSRSG--NQVSEVISNTFELDKQNEVEIPSTPRQRAFOQPPSV 78
QY 102 -----FRSIVHAVQAGIFVERMFRRTYSVGTPTSTAVLNCLKNLDLHCFDVF 149
Db 79 LRQSQPMQSQITGLKKLVHTGSLNTNVPRE-----GVKTDQEDLLAQELELSKGLNIF 132
QY 150 SLNQAAADHALRTIIVFELLTRHNLISRFKIPTVFLMSFLDALETGYGKYNPYHNOIHA 209
Db 133 CVSEYAGGRSLSCIMYTFQERDLLKKFHPVDVMMYMLTLEDHY-HADVAYHNSLHAA 191
QY 210 DVTQTVHCELLRTGMVHCLSEIELLAIIFAAAIHDEYHTGTTNSFHQTKSECAIYNDR 269
Db 192 DVLQSTHVLATPALDAVFTDLEILAAALFAAAIHVDHDPGVSNQFLINTNSLALWYND 251
QY 270 SVLENHHISSVFLRMQDDDMNIFINTKDEFVELRALVTEMVLATDMSCHFQVKTMTKA 329
Db 252 SVLENHHLAGVFKLLQEECDIFQNLKQROSLRKQKMWIDMVLATDMSKHMILLADLKT 311
QY 330 LQOLE-----RIDPKALSLLLHAADISHPTKQWLHVSRTWKALMEEFROGDK 378
Db 312 VETKVTSSGVLLLDNYSDRIOVLNMVHCADLSNPTKPLELYRQWTDRIAEFFQGDGR 371
QY 379 EAEALGLPSPCLDRSTLVAQSOIGFIDFIVEPTFSVLTDVAEKSVQPLAD--EDSKS-- 434
Db 372 ERERGMEISPMCKHTASVEKSVQGFIDYIVHPLWETWADLVHPDAQDILDTLEDNRD 431
QY 435 -----KNQPSFQWRQPSLDVE---VGDPN-PDVVSFRSTVWVKRIQEN 472
Db 432 HSAIROSPS-----PPEEPPGLGHPSLPDKFQFELTLEEEED 472
RESULT 14
B53109
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 4B, cAMP-specific, splice fcr
C:Species: Rattus norvegicus (Norway rat)
C:Date: 07-Jul-1995 #sequence revision 07-Jul-1995 #text_change 19-May-2000
C:Accession: B53109; A34414; C33904; I67944
R:Monaco, L.; Vicini, E.; Conti, M.
J. Biol. Chem. 269, 347-357, 1994
A:Title: Structure of two rat genes coding for closely related rolipram-sensitive cA
A:Reference number: A53109; MUID:94103234; PMID:8276818
A:Accession: B53109
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-584 <MON>
A:Cross-references: GB:U01280
R:Swinnen, J.V.; Joseph, D.R.; Conti, M.
Proc. Natl. Acad. Sci. U.S.A. 86, 8197-8201, 1989
A:Title: The mRNA encoding a high-affinity cAMP phosphodiesterase is regulated by hor
A:Reference number: A34414; MUID:90046763; PMID:2554303
A:Accession: A34414
A:Molecule type: mRNA
A:Residues: 1-584 <SWI>
A:Cross-references: GB:U09455; GB:M25349; NID:g517501; PIDN:AAA20401.1; PID:g517502;
R:Swinnen, J.V.; Joseph, D.R.; Conti, M.
Proc. Natl. Acad. Sci. U.S.A. 86, 5325-5329, 1989
A:Title: Molecular cloning of rat homologues of the Drosophila melanogaster dunce cA
A:Reference number: A33904; MUID:89315790; PMID:2546153
A:Accession: C33904
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 214-480 <SW2>
A:Cross-references: GB:M25349
R:Bolger, G.B.; Rodgers, L.K.; Riggs, M.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 10, 2003, 22:31:31 ; Search time 39 seconds
(without alignments)
622.199 Million cell updates/sec

Title: US-09-663-481-1
Perfect score: 2676
Sequence: 1 MANPVVQSHLQGLRLR.....EEAPPSPAEDEHNONGNLD 516

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2582	96.5	536	1 CN1B_HUMAN	Q01064 homo sapien
2	2491	93.1	535	1 CN1B_RAT	Q01066 rattus norv
3	2489	93.0	535	1 CN1B_MOUSE	Q01065 mus musculus
4	2484.5	92.8	534	1 CN1B_BOVIN	Q01061 bos taurus
5	1595	59.6	654	1 CN1C_MOUSE	Q64338 mus musculus
6	1594	59.6	768	1 CN1C_RAT	Q64321 rattus norv
7	1593	59.5	709	1 CN1C_HUMAN	Q14123 homo sapien
8	1591.5	59.5	529	1 CN1A_BOVIN	P14100 bos taurus
9	1575	58.9	565	1 CN1A_MOUSE	Q61481 mus musculus
10	1568.5	58.6	534	1 CN1A_HUMAN	P54750 homo sapien
11	1254.5	46.9	664	1 YFGK_CAEEL	O18696 caenorhabdi
12	638	23.8	549	1 YST1_CAEEL	Q22000 caenorhabdi
13	637	23.8	844	1 CN1C_MOUSE	O89084 mus musculus
14	630	23.5	712	1 CN1C_HUMAN	Q08493 homo sapien
15	622.5	23.3	844	1 CN1A_RAT	P54748 rattus norv
16	618	23.1	886	1 CN1A_HUMAN	P27815 homo sapien
17	617.5	23.1	809	1 CN1D_HUMAN	Q08499 homo sapien
18	616	23.0	536	1 CN1C_RAT	P14644 rattus norv
19	615	23.0	721	1 CN1B_RAT	P14646 rattus norv
20	613	22.9	736	1 CN1B_HUMAN	Q07343 homo sapien
21	612.5	22.9	672	1 CN1D_RAT	P14270 rattus norv
22	611	22.8	777	1 CN1A_DROME	P12252 drosophila
23	505	18.9	793	1 REGA_DICDI	Q23917 dictyosteli
24	481.5	18.0	799	1 CN1B_MOUSE	Q61409 mus musculus
25	481.5	18.0	1112	1 CN1B_HUMAN	Q13370 homo sapien
26	481.5	18.0	1141	1 CN1A_HUMAN	Q14432 homo sapien
27	478.5	17.9	1108	1 CN1B_RAT	Q63085 rattus norv
28	470.5	17.6	1141	1 CN1A_RAT	Q62865 rattus norv
29	467	17.5	446	1 CN1B_MOUSE	Q9q9x1 mus musculus
30	464	17.3	456	1 CN1A_MOUSE	P70453 mus musculus
31	461.5	17.2	426	1 CN1A_RAT	O08593 rattus norv
32	457.5	17.1	482	1 CN1A_HUMAN	Q13946 homo sapien
33	449	16.8	450	1 CN1B_HUMAN	Q9np56 homo sapien

RESULT 1

ID	CN1B_HUMAN	STANDARD	PRT	536 AA.
AC	Q01064	Q92825		
DE	01-APR-1993 (Rel. 25, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Calcium/calmodulin-dependent 3',5'-cyclic nucleotide phosphodiesterase 1B (EC 3.1.4.17) (Cam-PDE 1B) (63 kDa Cam-PDE).			
GN	PDE1B OR PDE1B1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97008163; PubMed=8855339;			
RA	Jiang X., Li J., Paskind M., Epstein P.M.;			
RT	"Inhibition of calmodulin-dependent phosphodiesterase induces apoptosis in human leukemic cells."			
RL	Proc. Natl. Acad. Sci. U.S.A. 93:11236-11241(1996).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=98081132; PubMed=9419816;			
RA	Yu J., Frazier A.L.B., Wolda S.L., Florio V.A., Martins T.J., Snyder P.B., Harris E.A.S., McCaw K.N., Farrell C.A., Steiner B., Bentley J.K., Beavo J.A., Ferguson K., Gelin R.;			
RT	"Identification and characterization of a human calmodulin-stimulated phosphodiesterase PDE1B1."			
RL	Cell. Signal. 9:519-529(1997).			
RN	[3]			
RP	SEQUENCE OF 222-337 FROM N.A.			
RX	MEDLINE=92406782; PubMed=1326532;			
RA	Repaske D.R., Swinnen J.V., Jin S.L.C., van Wyk J.J., Conti M.;			
RT	"A polymerase chain reaction strategy to identify and clone cyclic nucleotide phosphodiesterase cDNAs. Molecular cloning of the cDNA encoding the 63-kDa calmodulin-dependent phosphodiesterase."			
RL	J. Biol. Chem. 267:18683-18688(1992).			
CC	-!- FUNCTION: Has a preference for cGMP as a substrate.			
CC	-!- CATALYTIC ACTIVITY: Nucleoside 3',5'-cyclic phosphate + H(2)O -> nucleoside 5'-phosphate.			
CC	-!- ENZYME REGULATION: TYPE I PDE ARE ACTIVATED BY THE BINDING OF CALMODULIN IN THE PRESENCE OF CA(2+).			
CC	-!- SUBUNIT: Homodimer (By similarity).			
CC	-!- SUBCELLULAR LOCATION: Cytoplasmic.			
CC	-!- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE FAMILY.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			

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CC -----
DR EMBL; U56976; AAC50769.1; -
DR EMBL; U86078; AAC51872.1; -
DR EMBL; M94539; AAA58405.1; -
DR PIR; JC6129; JC6129.
DR PDB; 1LXR; 26-JUN-02.
DR Genew; HGNC:8775; PDE1B.
DR MIM; 171891; -.
DR GO; GO:0004117; F:calmodulin-dependent cyclic-nucleotide phos. . . ; TAS.
DR GO; GO:0006915; P:apoptosis; TAS.
DR InterPro; IPR003607; Met-phosphohydro.
DR TrEMBL; IPR002073; PDEase.
DR TrEMBL; IPR002073; PDEase.
DR SMART; SM00471; Hdc; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
KW Hydroxylase; cAMP; cGMP; Calmodulin-binding; 3D-structure.
FT DOMAIN 127 47 CALMODULIN-BINDING (POTENTIAL).
FT DOMAIN 197 496 CALMODULIN-BINDING (BY SIMILARITY).
FT CONFLICT 225 426 QI -> SM (IN REF. 2).
FT CONFLICT 337 337 S -> A (IN REF. 2).
SQ SEQUENCE 536 AA; 61379 MW; D15211AC32C756A4 CRC64;

Query Match
Best Local Similarity 96.5%; Score 2582; DB 1; Length 536;
Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

19 LRYMVKQLENGEINIEELKKNLEYTASLLEAVYIDETROIIDTEDELQELRSDAVPSEVR 78
|||||
39 LRYMVKQLENGEINIEELKKNLEYTASLLEAVYIDETROIIDTEDELQELRSDAVPSEVR 98
|||||
79 DWLASTFTQOARAKGRRAEKKPRRSIVHVAQAGIFVERMFRRTYTSVGTSTAVLNCL 138
|||||
99 DWLASTFTQOARAKGRRAEKKPRRSIVHVAQAGIFVERMFRRTYTSVGTSTAVLNCL 158
|||||
139 KNLDLWCFDVSFNQADDDHALRTIVFELLTRNLISRKPIPTVFLMSFLDALETGYGKY 198
|||||
159 KNLDLWCFDVSFNQADDDHALRTIVFELLTRNLISRKPIPTVFLMSFLDALETGYGKY 218
|||||
199 KNPYHNOIHAADVQTVHCFLLRTGVMVHCLSEIELLAIIPAAAIHDEYHGTGTSNPHIOT 258
|||||
219 KNPYHNOIHAADVQTVHCFLLRTGVMVHCLSEIELLAIIPAAAIHDEYHGTGTSNPHIOT 278
|||||
259 KSECAIYNDRSVLENHHISSVFRMLQDDENNIFNLTKDFVELRALVIEVLATDMSC 318
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279 KSECAIYNDRSVLENHHISSVFRMLQDDENNIFNLTKDFVELRALVIEVLATDMSC 338
|||||
319 HFQOVKTMKTALQQLERIDKPKALSLLHAADISHPTKQWLHRSRWTKALMEEFRRQGDK 378
|||||
339 HFQOVKTMKTALQQLERIDKPKALSLLHAADISHPTKQWLHRSRWTKALMEEFRRQGDK 398
|||||
379 EAEGLGPFSPCLDRTSTLVAQSQIGFIDFIVEPTFSVLTDAEKSVOPLADEDSKSNOP 438
|||||
399 EAEGLGPFSPCLDRTSTLVAQSQIGFIDFIVEPTFSVLTDAEKSVOPLADEDSKSNOP 458
|||||
439 SFQWRQPSLDVEYGDNDPVDVSPFRSTWVKRIQENKQWKERRAASGITNOMSIDELSPCEE 498
|||||
459 SFQWRQPSLDVEYGDNDPVDVSPFRSTWVKRIQENKQWKERRAASGITNOMSIDELSPCEE 518
|||||
499 EAPPSPAEDHNGNGLD 516
519 EAPPSPAEDHNGNGLD 536

```

RESULT 2

```

CNIB_RAT
ID CNIB_RAT STANDARD; PRT; 535 AA.
AC Q01066;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Calcium/calmodulin-dependent 3',5'-cyclic nucleotide phosphodiesterase
DE 1B (EC 3.1.4.17) (Cam-PDE 1B) (63 kDa Cam-PDE).
GN PDE1B OR PDE1B1.

```

```

OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=52406782; PubMed=1326532;
RA Repaske L.R., Swinnen J.V., Jin S.L.C., van Wyk J.J., Conti M.;
RT 'A polymerase chain reaction strategy to identify and clone cyclic
RT nucleotide phosphodiesterase cDNAs. Molecular cloning of the cDNA
RT encoding the 63-kDa calmodulin-dependent phosphodiesterase.';
RL J. Biol. Chem. 267:18683-18688(1992).
CC -1- CATALYTIC ACTIVITY: Nucleoside 3',5'-cyclic phosphate + H(2)O -
CC nucleoside 5'-phosphate.
CC -1- ENZYME REGULATION: TYPE I PDE ARE ACTIVATED BY THE BINDING OF
CC CALMODULIN IN THE PRESENCE OF CA(2+).
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
CC FAMILY.
CC -----
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch)
CC -----
CC EMBL; M94537; AAA16530.1; -
CC PIR; A44161; A44161.
CC InterPro; IPR003607; Met-phosphohydro.
CC InterPro; IPR002073; PDEase.
CC Pfam; PF00233; PDEase; 1.
CC SMART; SM00471; Hdc; 1.
CC PROSITE; PS00126; PDEASE_I; 1.
KW Hydroxylase; cAMP; cGMP; Calmodulin-binding.
FT DOMAIN 127 47 CALMODULIN-BINDING (POTENTIAL).
FT DOMAIN 196 495 CATALYTIC (BY SIMILARITY).
FT SEQUENCE 535 AA; 62259 MW; F98FFFE61F848F89 CRC64;

Query Match
Best Local Similarity 93.1%; Score 2491; DB 1; Length 535;
Matches 477; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

19 LRYMVKQLENGEINIEELKKNLEYTASLLEAVYIDETROIIDTEDELQELRSDAVPSEVR 78
|||||
38 LRYMVKQLENGEINIEELKKNLEYTASLLEAVYIDETROIIDTEDELQELRSDAVPSEVR 97
|||||
79 DWLASTFTQOARAKGRRAEKKPRRSIVHVAQAGIFVERMFRRTYTSVGTSTAVLNCL 138
|||||
98 DWLASTFTQOARAKGRRAEKKPRRSIVHVAQAGIFVERMFRRTYTSVGTSTAVLNCL 157
|||||
139 KNLDLWCFDVSFNQADDDHALRTIVFELLTRNLISRKPIPTVFLMSFLDALETGYGKY 198
|||||
158 KNLDLWCFDVSFNQADDDHALRTIVFELLTRNLISRKPIPTVFLMSFLDALETGYGKY 217
|||||
199 KNPYHNOIHAADVQTVHCFLLRTGVMVHCLSEIELLAIIPAAAIHDEYHGTGTSNPHIOT 258
|||||
218 KNPYHNOIHAADVQTVHCFLLRTGVMVHCLSEIELLAIIPAAAIHDEYHGTGTSNPHIOT 277
|||||
259 KSECAIYNDRSVLENHHISSVFRMLQDDENNIFNLTKDFVELRALVIEVLATDMSC 318
|||||
278 KSECAIYNDRSVLENHHISSVFRMLQDDENNIFNLTKDFVELRALVIEVLATDMSC 337
|||||
319 HFQOVKTMKTALQQLERIDKPKALSLLHAADISHPTKQWLHRSRWTKALMEEFRRQGDK 378
|||||
338 HFQOVKTMKTALQQLERIDKPKALSLLHAADISHPTKQWLHRSRWTKALMEEFRRQGDK 397
|||||
379 EAEGLGPFSPCLDRTSTLVAQSQIGFIDFIVEPTFSVLTDAEKSVOPLADEDSKSNOP 438
|||||
398 EAEGLGPFSPCLDRTSTLVAQSQIGFIDFIVEPTFSVLTDAEKSVOPLADEDSKSNOP 457

```


phosphodiesterase from bovine brain.";
 J. Biol. Chem. 267:18676-18682(1992).
 [2]
 PARTIAL SEQUENCE.
 TISSUE=Brain;
 RX MEDLINE=91329366; PubMed=1651112;
 RA Novack J.P., Charbonneau H., Bentley J.K., Walsh K.A., Beavo J.A.;
 "Sequence comparison of the 63-, 61-, and 59-kDa calmodulin-dependent
 cyclic nucleotide phosphodiesterases.";
 Biochemistry 30:7940-7947(1991).
 RL BIOCHEMISTRY 30:7940-7947(1991).
 CC -1- CATALYTIC ACTIVITY: Nucleoside 3',5'-cyclic phosphate + H(2O) =
 nucleoside 5'-phosphate.
 CC -1- ENZYME REGULATION: TYPE I PDE ARE ACTIVATED BY THE BINDING OF
 CALMODULIN IN THE PRESENCE OF CA(2+). REGULATED BY PHOSPHORYLATION
 BY CAM-DEPENDENT PROTEIN KINASE II.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN CENTRAL NERVOUS SYSTEM REGIONS.
 CC MOST ABUNDANT IN BASAL GANGLIA. ALSO FOUND IN KIDNEY PAPILLA
 AND ADRENAL MEDULA.
 CC -1- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
 FAMILY.

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 or send an email to license@isb-sib.ch).

 EMBL; M94867; AAA74558.1; -;
 PIR; A4162;
 InterPro; IPR003607; Met_Phsphohydro.
 DR InterPro; IPR002073; PDEase.
 DR Pfam; PF00223; PDEase; 1.
 DR PRINTS; PR00387; PD1ESTERASE1.
 DR SMART; SM00471; HDC; 1.
 DR PROSITE; PS00126; PDEASE_I; 1.
 DR KQ HYDROLASE; CAMP; CGMP; Phosphorylation; Calmodulin-binding.
 KW HYDROLASE; CAMP; CGMP; CALMODULIN-BINDING (POTENTIAL).
 FT DOMAIN 27 47
 FT DOMAIN 195 494
 FT SEQUENCE 534 AA; C86C3F48E0AE9B69 CRC64;
 SQ
 Query Match 92.88; Score 2484.5; DB 1; Length 534;
 Best Local Similarity 96.08; Pred No 1.9e-172;
 Matches 478; Conservative 10; Mismatches 9; Indels 1; Gaps 1;
 19 LRYMKQLENGEINIEELKNLEYTASLLEAVYIDEPTQILDEDELOELRSDAVPSEVR 78
 38 LRYMKQLENGEINIEELKNLEYTASLLEAVYIDEPTQILDEDELOELRSDAVPSEVR 97
 79 DWLASTTQOARAKGRRAEKPFRSIVHVOAGIFVERFRRTYTSVGPTYSTAVLNCL 138
 98 DWLASTTQOARAKGRRAEKPFRSIVHVOAGIFVERFRRTYTSVGPTYSTAVLNCL 156
 139 KNLDMCFDVFSLNQADHALRTIVFELLTRNLISRRKIPVFLMSFLDALETGYGY 198
 157 KNYDLNCFDVFSLNRAADHALRTIVFELLTRNLISRRKIPVFLMFLDALETGYGY 216
 199 KNPYHNIHAADVTQTVHCFLLRTGMVHCLSEIELLAIFAAAHIDYHGTGTTNSPHIQ 258
 217 KNPYHNIHAADVTQTVHCFLLRTGMVHCLSEIELLAIFAAAHIDYHGTGTTNSPHIQ 276
 259 KSECAIYNDRSVLENNHHSVFLRMQDDMMNIFINLTDFVELRALVEMVLAIDMSC 318
 277 KSECAIYNDRSVLENNHHSVFLRMQDDMMNIFINLTDFVELRALVEMVLAIDMSC 336
 319 HFQOVKMTALQOOLERIDPKALSLLLHAADISHTPKWLVSRRTKALMEFFRQGD 378
 337 HFQOVKMTALQOOLERIDSKALSLLLHAADISHTPKWLVSRRTKALMEFFRQGD 396
 379 EAEGLPFPCLCDRTSTLVAQSQIGFDIFVEFTFVLTDVAEKSVQPTGDDSKSNQP 438

Db 397 EAEGLPFPCLCDRTSTLVAQSQIGFDIFVEFTFVLTDVAEKSVQPTGDDSKSNQP 456
 Qy 439 SFQWRQPSLDVEGDPNPDVVVSRSTWVKRQENKQKWKRAASGITNQMISIDELSPCEE 498
 Db 457 SFQWRQPSLDVEGDPNPDVVVSRSTWVKRQENKQKWKRAASGITNQMISIDELSPCEE 516
 Qy 499 EAPSPAEDEHNQNGNLD 516
 Db 517 EAPSPAEDEHNQNGNLD 534

RESULT 5
 CNIC_MOUSE
 ID CNIC_MOUSE STANDARD; PRT; 654 AA.
 AC Q64338; Q62045;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Calcium/calmodulin-dependent 3',5'-cyclic nucleotide phosphodiesterase
 DE 1C (EC 3.1.4.17) (Cam-PDE 1C).
 GN PDE1C.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RC SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RX STRAIN=BALB/c; TISSUE=Brain;
 MEDLINE=96411795; PubMed=8810348;
 RA Yan C., Zhao A.Z., Bentley J.K., Beavo J.A.;
 "The calmodulin-dependent phosphodiesterase gene PDE1C encodes
 several functionally different splice variants in a tissue-specific
 manner.";
 RT J. Biol. Chem. 271:25699-25706(1996).
 RL J. Biol. Chem. 271:25699-25706(1996).
 CC -1- FUNCTION: HIGH AFFINITY CAMP AND CGMP CALMODULIN-DEPENDENT
 PHOSPHODIESTERASE
 CC -1- CATALYTIC ACTIVITY: Nucleoside 3',5'-cyclic phosphate + H(2O) =
 nucleoside 5'-phosphate.
 CC -1- ENZYME REGULATION: TYPE I PDE ARE ACTIVATED BY THE BINDING OF
 CALMODULIN IN THE PRESENCE OF CA(2+).
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Even-Alternative splicing; Named isoforms=2;
 CC Comment-Additional isoforms seem to exist;
 CC Name=1; Synonyms=PDE1C4, PDE1C5;
 CC IsoId=Q64338-1; Sequence=Displayed;
 CC Name=2; Synonyms=PDE1C1;
 CC IsoId=Q64338-2; Sequence=VSP_004554;
 CC TISSUE SPECIFICITY: Isoform 1 is highly expressed in testis.
 CC Isoform 2 is highly expressed in heart and testis, and detected at
 CC lower levels in olfactory epithelium and cerebellum.
 CC -1- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
 FAMILY.

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 or send an email to license@isb-sib.ch).

 EMBL; L75947; AAC37702.1; -;
 EMBL; L75946; AAC37703.1; -;
 EMBL; L75944; AAC37701.1; -;
 MGD; MGI:109413; Pde1c.
 DR InterPro; IPR003607; Met_Phsphohydro.
 DR InterPro; IPR002073; PDEase.
 DR Pfam; PF00223; PDEase; 1.
 DR PRINTS; PR00387; PD1ESTERASE1.
 DR SMART; S400471; HDC; 1.
 DR PROSITE; PS00126; PDEASE_I; 1.

78	DWLASTFTQARAKGRRAEKEPKFRSIHVAOAGIFVERMFRRTVTSVGPTSYAVLNC	133
DB	: : : : : : : :	
103	RDLASTFTROMGMLRRSDEKPRFSIHVAOAGIFVERMYRRTSNMVLSPYPAVIEA	162
DB	: : : : : : : :	
138	LKNLDLCWFDFSLNQAADHALRTIVFELLTRHNLSIRFKPTPVFLMSFLDALETGYK	197
DB	: : : : : : : :	
163	LKDWDKSFDFSLNEASGDHALKFYPVELLTVDLSIRFKPIPSALSVFVEALEVGYSK	222
DB	: : : : : : : :	
198	TKNPYHQIHAADVTQVHVCHLLRTGMVHCISLEILLAIIFAAAIHDIYHTGTTFNSFHQ	257
DB	: : : : : : : :	
223	EKNPYHNLMAAADVTQVHVLLKYGVANWLTELEIFALIFSAAIHDIYHTGTTNNFHQ	282
DB	: : : : : : : :	
258	TKSCAIVNDRSVLENHHISSVFRLMODD-ENNIFINTKDEFELRALVIEMVLATDM	316
DB	: : : : : : : :	
283	TRSDPAILYNDRSVLENHHLSSAYRLLQLDDDEMNILINLKKDDREFRTLVIEMVATDM	342
DB	: : : : : : : :	
317	SCHFQQVKMTKTAQLOOLERTDKPKALSLLLHAADISHPTKOWLVHSRWTKALMEFFRQG	376
DB	: : : : : : : :	
343	SCHFQQIKAMKTALOQPEALEKPKALSMLHTADISHPAKAMDLLHRWTMSLLEEFFRQG	402
DB	: : : : : : : :	
377	EKEAEGLGPSPLCDRSTVLVASQSIGTDFIVEPTFSVLTDVAEKSVOPLADEDSKKN	436
DB	: : : : : : : :	
403	EKEAEGLGPSPLCDRSTWVASQSGVIDFIVEPTFTVLDTMKETKISPLDIDETSQGG	462
DB	: : : : : : : :	
437	QPSFWQRQPSLD-VEVGDP-----NDPVVSFRSTWVKRKIQENKK	474
DB	: : : : : : : :	
463	TGQ---RKSUNLSSISSDAKRSKVKGSGSGSAPINNVSIVDYKFSKATVTEVVHINRE	519
DB	: : : : : : : :	
475	XWKERAAAGITNQMSIDELSPCEEEAPPSPA E 506	
DB	: : : : : : : :	
520	XWRKRV-----PKERAKKEAEE 537	
DB	: : : : : : : :	
RESULT 8		
CNIA_BOVIN		
ID CNIA_BOVIN STANDARD; PRT; 529 AA.		
P14100; Q82063;		
01-JAN-1930 (Rel. 13, Created)		
01-JUN-1934 (Rel. 29, Last annotation update)		
15-SEP-2033 (Rel. 42, Last annotation update)		
Calcium/calmodulin-dependent 3',5'-cyclic nucleotide phosphodiesterase		
1A (EC 3.1.4.17) (Cam-PDE 1A) (61 kDa Cam-PDE).		
PDE1A.		
Bos taurus (Bovine).		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;		
Bovidae; Bovinae; Bos.		
NCBI_TaxID=9913;		
[1]		
SEQUENCE (ISOFORM 2).		
TISSUE=Brain;		
MEDLINE=91329365; PubMed=1651111;		
Charbonneau H., Kumar S., Norack J.P., Blumenthal D.K., Griffin P.R.,		
Shabarova Z.J., Hunt D.F., Beavo J.A., Walsh K.A.;		
"Evidence for domain organization within the 61-kDa calmodulin-		
dependent cyclic nucleotide phosphodiesterase from bovine brain."		
Biochemistry 30:7931-7940(1991).		
[2]		
SEQUENCE FROM N.A.		
TISSUE=Brain;		
MEDLINE=93107074; PubMed=7678006;		
Charbonneau W.K., Seger D., Beavo J.A.;		
"Molecular cloning of a cDNA encoding the '61-kDa' calmodulin-		
stimulated cyclic nucleotide phosphodiesterase. Tissue-specific		
expression of structurally related isoforms."		
J. Biol. Chem. 268:645-652(1993).		
[3]		
SEQUENCE FROM N.A. (ISOFORM 1).		
TISSUE=Lung;		
MEDLINE=93125075; PubMed=8537356;		
Charbonneau W.K., Seger D., Kwak K.S., Huang J., Charbonneau H.,		
Beavo J.A.;		
"Identification of inhibitory and calmodulin-binding domains of the		

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RT PDE1A1 and PDE1A2 calmodulin-stimulated cyclic nucleotide
RT phosphodiesterases."
RL J. Biol. Chem. 270:30989-31000(1995).
RN [4]
RP SEQUENCE OF 193-426.
RC TISSUE=Brain;
RX MEDLINE=87092242; PubMed=3025833;
RA Charbonneau H., Beier N., Walsh K.A., Beavo J.A.;
RT "Identification of a conserved domain among cyclic nucleotide
RT phosphodiesterases from diverse species."
RL Proc. Natl. Acad. Sci. U.S.A. 83:9308-9312(1986).
CC -!- CATALYTIC ACTIVITY: Nucleoside 3',5'-cyclic phosphate + H(2)O -
CC nucleoside 5'-phosphate.
CC -!- ENZYME REGULATION: TYPE I PDE ARE ACTIVATED BY THE BINDING OF
CC CALMODULIN IN THE PRESENCE OF CA(2+).
CC -!- SUBUNIT: Homodimer.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms-2;
CC Name=2; Synonyms=PDE1A2;
CC IsoId=PI4100-1; Sequence=Displayed;
CC Name=1; Synonyms=PDE1A1;
CC IsoId=PI4100-2; Sequence=VSP_004546;
CC -!- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
CC FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M90358; AAA74560.1; -
DR EMBL; L34069; AAA92555.1; -
DR PIR; A45334; A45334.
DR InterPro; IPR003607; Met_phosphohydro.
DR Pfam; PF00233; PDEase; 1.
DR SMART; SM00471; Hdc; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
KW Hydrolase; CAMP; cGMP; Multigene family; Alternative splicing;
KW Calmodulin-binding.
FT INIT_MET 0 0
FT DOMAIN 23 43 CALMODULIN-BINDING.
FT FT 500 CATALYTIC (BY SIMILARITY).
FT FT 192 GSTRATELENTTEFKYLIGGOTKMWQLKGI -> MDDH
FT VARSPLIC 1 33 VTIRKHLQRPFR (in isoform 1).
FT FT /FTIG-VSP_004546.
FT CONFLICT 236 236 H -> G (IN REF. 4).
FT CONFLICT 320 320 N -> W (IN REF. 4).
SQ SEQUENCE 529 AA; 60712 MW; 24DB74C22A2AE06F CRC64;

Query Match 59.5%; Score 1591.5; DB 1; Length 529;
Best Local Similarity 61.2%; Pred. No. 8.4e-108;
Matches 300; Conservative 91; Mismatches 90; Indels 9; Gaps 1;

QY 19 LRYMYKQLENGEINTEELKKNLEYTASLLEAVYIDETQILDTEDELRSAYPSEVR 78
DB 34 LRLCYKQLEKGVNVVIDKKNIEYAAVLEAVYIDETRLRLDDELSDIQSDVSEVR 93
QY 79 DWLASTFTQARAKGRRAEKPFRSIVHVOAGIFVERMPRTYTSVGPYSTAVLACL 138
DB 94 DWLASTFTFKGMKMKKEEKPFRSIVHVOAGIFVERWKRKSHVMGLAYPEAVITL 153
QY 139 KNLDLWCDFVSLNQAADHALRTIVFELLTRHNLISRFKPTVFPLMSFLDALETGYKY 198
DB 154 KDVDKWSDEVFALNEASGHSLSKFMVIELETRYDLINRKIPVSCILFAFALEAVGYSKY 213
QY 199 KNPYHQNHAAVDVTQVHCFLRTGHWCHLSIELLALIFAAAHIDYEHGTNTSFHIQT 258
DB 214 KNPYHNLHAAVDVTQVHYIMLHTGIMHWLTELILAMVFAAAHIDYEHGTNTSFHIQT 273
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QY 259 KSECAIVNDRSVLENHHISSVFLRMQDDEMNIFNLTKDEFVELRALVIEVLATDMSC 318
DB 274 RSDVAILYNDRSVLENHHVSAAYRLMQEENNVNLINLSKDDWRDLRLNLVIEVLSTDMSG 333
QY 319 HFQVQVTKMTALQQLERIDKPKALSLLLHAADISHPTQKWLHVSHWTALMEEFPRQGDK 378
DB 334 HFQQIKNIRNSLQPEGLDKARTMSLILHAADISHPAKSWKLHHRWTALMEEFLOGDK 393
QY 379 EAEGLPSPICLDRSTLVAQSQIGFIDFIVEPTESVLTDVAEKSVQPLADEDSKKNOP 438
DB 394 EAEGLPSPICLDRKSTWVAQSQIGFIDFIVEPTESLTDSTEKIIILIEDSKTKTPS 453
QY 439 SFQWRQPSLDVEVGD-----PNDVVSFRSTWVKRIQENKOKKERAASGTTNOMS 489
DB 454 YGASRRSNMKGTTNDGTYSPOYSLASVDLKSFKNSLVLDIQONKRWKELAAQGPDPHK 513
QY 490 IDELSPCEEE 499
DB 514 NSDLVNAEEK 523

RESULT 9
CNIA_MOUSE STANDARD; PRT; 565 AA.
ID CNIA_MOUSE
AC Q61481; O35388;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Calcium/calmodulin-dependent 3',5'-cyclic nucleotide phosphodiesterase
DE 1A (EC 3.1.4.17) (Cam-PDE 1A) (61 kDa Cam-PDE).
GN PDE1A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_taxid=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM PDE1A2).
RC STRAIN=BALB/c; TISSUE=Brain;
RA Yan C., Sonnenburg W.K., Zhao A.Z., Kwak K.S., Beavo J.A.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE OF 1-262 FROM N.A. (ISOFORM PDE1A1).
RC TISSUE=Heart;
RA Sonnenburg W.K., Rybalkin S.D., Bornfeldt K.E., Kwak K.S.,
RA Rybalkina I., Beavo J.A.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: HAS A HIGHER AFFINITY FOR CGMP THAN FOR CAMP.
CC -!- CATALYTIC ACTIVITY: Nucleoside 3',5'-cyclic phosphate + H(2)O -
CC nucleoside 5'-phosphate.
CC -!- ENZYME REGULATION: TYPE I PDE ARE ACTIVATED BY THE BINDING OF
CC CALMODULIN IN THE PRESENCE OF CA(2+).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms-2;
CC Name=PDE1A2;
CC IsoId=Q61481-1; Sequence=Displayed;
CC Name=PDE1A1;
CC IsoId=Q61481-2; Sequence=VSP_004551;
CC -!- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
CC FAMILY.
CC -----
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CC -----
DR EMBL; U56649; AAB03319.1; -
DR EMBL; AF023529; AAB81952.1; -
DR MGI; 1201792; Pdela.
DR InterPro; IPR003607; Met_phosphohydro.
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Db 420 NSLHADVLQSTVLLATPALDAVFTDLELALFAAAIHVDHVGVSNOFLINTSELA 479
Qy 264 IVYNDSEVLEHHISSVRLVMDENWIFNLKDFEVALRALVIEWLATDMSCHFOQV 323
Db 480 LKYNDESVLEHHILANGVFLQGECDIFQNLKQROSLKRWIVDMVLADMSKMTLL 539
Qy 324 KTKMTALOOLE-----RIDPKALSLILLHAADISHPTKQWLIVSRWTKALMEEF 372
Db 540 ADKWTYETKTKVTSVGVLNDYSDRIQVLRNMVHCADLSNPPLKLELYQWTDRIWAEF 599
Qy 373 FROGDEAEGLFPLCSDRTSLTVAQSQIGTFIDFVEPTFSLTVDVAEKSVQPLAD--E 430
Db 600 FQGDREERERMEISCMCKHTASVEKSVQGFIDYIVHPLWETWADLVHPDAQDILDTLE 659
Qy 431 DSKS-----KNPSPFWOPROPSLDVEVG---DPN-PDVVSFRSTWTKRIQNKQWKERA 480
Db 660 DNRDWHYSAIRQSPS-----PTLEEPGVLSDPALPKFOFEL-----LEEDEE----- 705
Qy 481 ASGITNQMSIDELSPCEEAPPSP 504
Db 706 -----DSLEVPGL-PCTEETLLAP 723

RESULT 14

CN4C_HUMAN
ID CN4C_HUMAN STANDARD; PRT; 712 AA.
AC Q08493; Q9UN44; Q9UN45; Q9UN46; Q9UPJ6;
DT 01-OCT-1996 (Rel. 34, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE CAMP-specific 3',5'-cyclic phosphodiesterase 4C (EC 3.1.4.17)
DE (PDE1) (PDE21).
GN PDE4C.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM PDE4C1).
RC TISSUE=Substantia nigra;
RX MEDLINE=95145731; PubMed=7843419;
RA Engels P., Sullivan M., Mueller T., Luebbert H.;
RT "Molecular cloning and functional expression in yeast of a human
RT CAMP-specific phosphodiesterase subtype (PDE IV-C).";
RL FEBS Lett. 358:303-310(1995).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS PDE4C1; PDE4C2 AND PDE4C3).
RX MEDLINE=20039485; PubMed=10574328;
RA Sullivan M., Olsen A.S., Houslay M.D.;
RT "genomic organisation of the human cyclic AMP-specific
RT phosphodiesterase PDE4C gene and its chromosomal localisation to
RL 19p13.1, between RAB3A and RUND.";
RL Cell. Signal. 11:735-742(1999).
RN [3]
RP SEQUENCE FROM N.A.
RA Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,
RA Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stillwagen S.,
RA Phan H., Velasco N., Do L., Regala W., Terry A., Ganes J.,
RA Danganan L., Poundstone P., Christensen M., Georgescu A., Avila J.,
RA Liu S., Attix C., Andreise T., Trankheim M., Amico-Keller G.,
RA Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,
RA Crommiller B., Arellano A., Saunders C., Ow D., Nolan M., Trong S.,
RA Kobayashi A., Olsen A.S., Carrano A.V.;
RT "Sequence analysis of an ~600 kb region in 19p13.1 between JAK3 and
RT PDE4C.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 462-712 FROM N.A.
RX MEDLINE=94019330; PubMed=8413254;
RA Bolger G., Michaeli T., Martins T., St John T., Steiner B.,
RA Rodgers L., Riggs M., Wigler M., Ferguson K.;
RT "A family of human phosphodiesterases homologous to the duncce

learning and memory gene product of Drosophila melanogaster are
potential targets for antidepressant drugs.";
Mol. Cell. Biol. 13:6558-6571(1993).
CC -!- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O ->
CC adenosine 5'-phosphate.
CC -!- ENZYME REGULATION: INHIBITED BY ROLIPRAM.
CC -!- PATHWAY: Cyclic nucleotide metabolism.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=PDE4C1;
CC Name=PDE4C1;
CC IScID=Q08493-1; Sequence=Displayed;
CC Name=PDE4C2;
CC IScID=Q08493-2; Sequence=VSP_004575;
CC Name=PDE4C3;
CC IScID=Q08493-3; Sequence=VSP_004574;
CC Name=PDE4C4;
CC IScID=Q08493-4; Sequence=Not described;
CC Name=PDE4C5;
CC IScID=Q08493-5; Sequence=Not described;
CC Name=PDE4C6;
CC IScID=Q08493-6; Sequence=Not described;
CC Name=PDE4C7;
CC IScID=Q08493-7; Sequence=Not described;
CC -!- TISSUE SPECIFICITY: EXPRESSED IN VARIOUS TISSUES BUT NOT IN CELLS
CC OF THE IMMUNE SYSTEM.
CC -!- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
CC FAMILY.
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CC EMBL: AF157811; AAD47053.1; JOINED.
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[3] SEQUENCE FROM N.A. (ISOFORM 2).
 RP STRAIN-Sprague-Dawley; TISSUE-Testis;
 RX MEDLINE=961132847; PubMed=8557632;
 RA Bolger G.B., McPhee I., Houslay M.D.;
 RT "Alternative splicing of cAMP-specific phosphodiesterase mRNA
 transcripts. Characterization of a novel tissue-specific isoform,
 RNPDS4A8.";
 RT J. Biol. Chem. 271:1065-1071(1996).
 RL [4]
 RP SEQUENCE OF 319-677 FROM N.A. (ISOFORM 3/4).
 RC TISSUE-Testis;
 RX MEDLINE=893115790; PubMed=2546153;
 RA Swinnen J.V., Joseph D.R., Conti M.;
 RT "Molecular cloning of rat homologs of the Drosophila melanogaster
 dunce cAMP phosphodiesterase: evidence for a family of genes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:5325-5329(1989).
 RN [5]
 RP STRUCTURE BY NMR OF 1-26 OF ISOFORM 3.
 RX MEDLINE=96279244; PubMed=8663181;
 RA Smith K.J., Scotland G., Beattie J., Trayer I.P., Houslay M.D.;
 RT "Determination of the structure of the N-terminal splice region of
 the cyclic AMP-specific phosphodiesterase RD1 (RNPDS4A1) by 1H NMR
 and identification of the membrane association domain using chimeric
 constructs.";
 RL J. Biol. Chem. 271:16703-16711(1996).
 CC -1- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O =
 CC adenosine 5'-phosphate.
 CC -1- ENZYME REGULATION: Inhibited by rolipram.
 CC -1- PATHWAY: Cyclic nucleotide metabolism.
 CC -1- ALTERNATIVE PRODUCTS:
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 CC Name=2; Synonyms=PDE4A8;
 CC IsoId=P54748-2; Sequence=VSP_004565;
 CC Name=3;
 CC IsoId=P54748-3; Sequence=VSP_004566, VSP_004567;
 CC Name=4; Synonyms=Medium;
 CC IsoId=P54748-4; Sequence=VSP_004568;
 CC Name=5; Synonyms=Short;
 CC IsoId=P54748-5; Sequence=VSP_004569, VSP_004570;
 CC -1- TISSUE SPECIFICITY: ISOFORM 2 IS PRESENT ONLY IN TESTIS.
 CC -1- SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
 CC FAMILY.
 CC -----
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OM protein - protein search, using sw model

Run on: August 11, 2003, 00:48:06 ; Search time 70 seconds
(without alignments)
1902.216 Million cell updates/sec

Title: US-09-663-481-1
Perfect score: 2676
Sequence: 1 MANPVPVQSHLQGPILRLR.....EEAPPSPAEHNGNGLD 516

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23:.*
1: sp.archaea.*
2: sp.bacteria.*
3: sp.fungi.*
4: sp.human.*
5: sp.invertebrate.*
6: sp.mammal.*
7: sp.mhc.*
8: sp.organelle.*
9: sp.phage.*
10: sp.plant.*
11: sp.rodent.*
12: sp.virus.*
13: sp.vertibrate.*
14: sp.unclassified.*
15: sp.virus.*
16: sp.bacteriap.*
17: sp.archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
1	2676	100.0	516	4	Q96KP3	Q96kp3 homo sapien
2	2349	95.3	536	6	Q9BE16	Q9be16 macaca fasc
3	2473	92.4	495	11	Q9DBS6	Q9db56 mus musculus
4	1626.5	60.8	515	6	Q95NB8	Q95nb8 canis famli
5	1618	60.5	529	4	Q9COL0	Q9c010 homo sapien
6	1616.5	60.4	536	4	Q9COL4	Q9c014 homo sapien
7	1595	59.6	603	11	Q8CDV2	Q8cdv2 mus musculus
8	1593	59.6	706	11	Q8BSV6	Q8bsv6 mus musculus
9	1593	59.5	617	11	Q9DSW0	Q9dsw0 mus musculus
10	1589	59.5	634	4	Q8TAE4	Q8tae4 homo sapien
11	1589	59.4	769	4	Q8NB10	Q8nb10 homo sapien
12	1575	58.9	545	11	Q8BRE9	Q8br9 mus musculus
13	1551.5	58.0	542	11	Q9EPR9	Q9ep9 rattus norv
14	1432	53.5	511	4	Q9C0K8	Q9c0k8 homo sapien
15	1431.5	53.5	456	11	Q9JLL9	Q9jll9 mus musculus
16	1430.5	53.5	518	4	Q9C0L2	Q9c0l2 homo sapien

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17 1424.5 53.2 501 4 Q9COL1
18 1149.5 43.0 605 5 Q9VKE9
19 1143.5 42.7 834 5 Q8XRO
20 999 37.3 199 11 Q64395
21 948 35.4 184 4 Q16713
22 855 32.0 628 5 Q96075
23 638 23.8 599 5 Q8IF23
24 638 23.8 626 5 Q95206
25 631 23.6 700 4 P78505
26 630 23.5 782 4 Q76105
27 630 23.5 791 4 Q43849
28 629 23.5 518 4 Q43850
29 622.5 23.3 584 11 Q8C4Q7
30 622.5 23.3 771 11 Q9EQR7
31 622 23.2 426 4 Q9UPJ5
32 617.5 23.1 518 4 Q8IVD3
33 617.5 23.1 748 4 Q8IVD2
34 617 23.1 521 5 Q8MRN3
35 617 23.1 624 5 Q9W4S8
36 617 23.1 629 5 Q8IRU5
37 617 23.1 642 5 Q8IRU6
38 617 23.1 662 5 Q8IRU4
39 617 23.1 711 5 Q8IRU7
40 617 23.1 776 5 Q8IRU8
41 617 23.1 778 5 Q8IRU9
42 617 23.1 1070 5 Q8IRV0
43 617 23.1 1209 5 Q8MS17
44 617 23.1 1209 5 Q8IRV1
45 616.5 23.0 687 4 Q8IV84

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ALIGNMENTS

RESULT 1

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Q96KP3 PRELIMINARY; PRT; 516 AA.
AC Q96KP3;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE 3'5' cyclic nucleotide phosphodiesterase 1B2.
GN PDE1B2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Testis;
RA Fidock M.D., Miller M., Lanfear J.;
RT "Isolation and differential tissue distribution of two human cDNAs
encoding PDE1 splice variants."
RL "Cell. Signal. 14:53-60(2001)."
DR EMBL; AJ401609; CAC82207.1;
DR InterPro; IPR003607; Met.phsphohydro.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF00233; PDEase; 1.
DR PRINTS; PR00387; PD1ESTERASE1.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE-1;
SQ SEQUENCE 516 AA: 59051 MW; 0A9093462479DC5C CRC64;

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Query Match 100.0%; Score 2676; DB 4; Length 516;
Best Local Similarity 100.0%; Pred. No. 2.8e-206;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MANPVPVQSHLQGPILRLRYMVVKOLENGEINIEELKKNLEVTASLLAEVYIDETQRLD 60
Db 1 MANPVPVQSHLQGPILRLRYMVVKOLENGEINIEELKKNLEVTASLLAEVYIDETQRLD 60
QY 61 TEDELQELRSDAVPSEVRDNLASTTQQAARAKGRAEKPFRSIVHVAQAGIFVERMFR 120
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Db 61 TEDELQELSDAVPSEVRDHLASTFTQQAARAGRRAEKPKERSIVHVAQAGIFVERMFR 120
 QY 121 RYTVSGPYSTAVLNCNLDWCDDVSLNQADDDHALRTIVFELLTRHNLISRFKIP 180
 Db 121 RYTVSGPYSTAVLNCNLDWCDDVSLNQADDDHALRTIVFELLTRHNLISRFKIP 180
 QY 181 TVFLMSFLDALETGYGKYKNPNHQNQIHAADVTQTVHCFLLRTGMVHCLSEIELLAIIFAA 240
 Db 181 TVFLMSFLDALETGYGKYKNPNHQNQIHAADVTQTVHCFLLRTGMVHCLSEIELLAIIFAA 240
 QY 241 AIHDEYHTGTTNSFHIOKSECAIYVNDRSVLNHHISSVFRMLQDDENMIFINTKDFE 300
 Db 241 AIHDEYHTGTTNSFHIOKSECAIYVNDRSVLNHHISSVFRMLQDDENMIFINTKDFE 300
 QY 301 VELRALVIEMLVATDMSCHFSQVQVTKMTALQOQLERIDKPKALSLLLHAADISHPTKQWLV 360
 Db 301 VELRALVIEMLVATDMSCHFSQVQVTKMTALQOQLERIDKPKALSLLLHAADISHPTKQWLV 360
 QY 361 HSRWTKALMEEFROQDKAEELGLPSPCLDRTSTLVAQSQIGFIDFIVEPTFSLTQVA 420
 Db 361 HSRWTKALMEEFROQDKAEELGLPSPCLDRTSTLVAQSQIGFIDFIVEPTFSLTQVA 420
 QY 421 EKSVPOLADEDSKSNOPSFQWRQPSLDVEGDPNDPVVFSRSTWVKRIQENKQKWKERA 480
 Db 421 EKSVPOLADEDSKSNOPSFQWRQPSLDVEGDPNDPVVFSRSTWVKRIQENKQKWKERA 480
 QY 481 ASGITNQMIDELSPCEEAPSPAEDEHNQNLID 516
 Db 481 ASGITNQMIDELSPCEEAPSPAEDEHNQNLID 516

RESULT 2

Q9DBS6 PRELIMINARY; PRT: 536 AA.
 AC Q9DBS6
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Hypochemical 61.4 kDa protein.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
 OC Cercopitheinae; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Frontal cortex;
 RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
 RA Suzuki Y., Sugano S., Hashimoto K.;
 RT "Isolation of full-length cDNA clones from macaque brain cDNA
 libraries";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB060237; BAB41164.1;
 DR InterPro: IPR003607; Met_phosphohydro.
 DR Pfam: PF00233; PDEase.
 DR PRINTS: PR00387; PDIESTERASE1.
 DR SMART: SM00471; HDC; 1
 DR PROSITE: PS00126; PDEASE_I; 1.
 KW Hypothetical protein
 SQ SEQUENCE 536 AA; 61364 MW; 5B0F82829574B9C6 CRC64;

Query Match 95.3%; Score 2549; DB 6; Length 536;
 Best Local Similarity 98.0%; Pred. No. 4.6e-196;
 Matches 488; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 19 LRYMKVQLNGEINTEELKKNLEYTASLEAVYIDETROIILDEQLRSDAVPSEVR 78
 Db 39 LRYMKVQLNGEINTEELKKNLEYTASLEAVYIDETROIILDEQLRSDAVPSEVR 98
 QY 79 DWLASTFTQQAARAGRRAEKPKERSIVHVAQAGIFVERMFRRTYTSVGYTSTAVLNCL 138
 Db 99 DWLASTFTQQAARAGRRAEKPKERSIVHVAQAGIFVERMFRRTYTSVGYTSTAVLNCL 158

QY 139 KNLDWCDDVSLNQADDDHALRTIVFELLTRHNLISRFKIPTVFLMSFLDALETGYKY 198
 Db 139 KNLDWCDDVSLNQADDDHALRTIVFELLTRHNLISRFKIPTVFLMSFLDALETGYKY 218
 QY 199 KNPYHQNQIHAADVTQTVHCFLLRTGMVHCLSEIELLAIIFAAIHDYHTGTTNSFHIO 258
 Db 219 KNPYHQNQIHAADVTQTVHCFLLRTGMVHCLSEIELLAIIFAAIHDYHTGTTNSFHIO 278
 QY 259 KSECAIYVNDRSVLNHHISSVFRMLQDDENMIFINTKDFEVELRALVIEMLVATDMS 318
 Db 279 KSECAIYVNDRSVLNHHISSVFRMLQDDENMIFINTKDFEVELRALVIEMLVATDMS 338
 QY 319 HFQVQVTKMTALQOQLERIDKPKALSLLLHAADISHPTKQWLVHSRWTALMEEFROQDK 378
 Db 339 HFQVQVTKMTALQOQLERIDKPKALSLLLHAADISHPTKQWLVHSRWTALMEEFROQDK 398
 QY 379 EAEGLPSPCLDRTSTLVAQSQIGFIDFIVEPTFSLTQVAEKSVQPLADEDSKSNOP 438
 Db 399 EAEGLPSPCLDRTSTLVAQSQIGFIDFIVEPTFSLTQVAEKSVQPLADEDSKSNOP 458
 QY 439 SFQWRQPSLDVEGDPNDPVVFSRSTWVKRIQENKQKWKERAASGITNQMIDELSPCEE 498
 Db 459 SFQWRQPSLDVEGDPNDPVVFSRSTWVKRIQENKQKWKERAASGITNQMIDELSPCEE 518
 QY 499 EAPSPAEDEHNQNLID 516
 Db 519 EAPSPAEDEHNQNLID 536

RESULT 3

Q9DBS6 PRELIMINARY; PRT: 495 AA.
 AC Q9DBS6
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Adult male lung cDNA, RIKEN full-length enriched library.
 DE clone:120014008, full insert sequence.
 GN PDE1B OR PDE1B1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Lung;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido T., Pesole C., Quackenbush J.,
 RA Schriml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baidarelli R., Barsh G.,
 RA Blake J., Boirelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamliya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mommaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki E., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki E., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 DR EMBL: AF004772; BAB23551.1;
 DR MGD: MG1:97523; Pde1b.
 DR InterPro: IPR003607; Met_phosphohydro.
 DR InterPro: IPR002073; PDEase.
 DR Pfam: Pf00233; PDEase; 1.

DR PRINTS; PR00387; PD1ESTERASE1.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
SQ SEQUENCE 495 AA; 56598 MW; FB86B38967CFD0C4 CRC64;

Query Match 92.4%; Score 2473; DB 11; Length 495;
Best Local Similarity 95.8%; Pred. No. 5.2e-190;
Matches 474; Conservative 12; Mismatches 9; Indels 0; Gaps 0;

QY 22 MVKOLENGEINIEELKKLEYTASLLEAVYIDETRIQILDTEDEQLERSDAVPSVRDL 81
DQ 1 MVKOLENGEVNIEELKKLEYTASLLEAVYIDETRIQILDTEDEQLERSDAVPSVRDL 60
QY 82 ASTTQARAKGRAEERPKERSIVHVAQAGIFVERMERFRTYTSVGTSTAVLNCKNL 141
DQ 61 ASTTQOTRAGRAREERPKERSIVHVAQAGIFVERMERFRTYTSVGTSTAVLNCKNL 120
QY 142 DLWCFDVFSLNQAADHALRTIVFELLTRHNLISRFKIPTVFLMSFLDALETGYGKYNP 201
DQ 121 DLWCFDVFSLNQAADHALRTIVFELLTRHNLISRFKIPTVFLMSFLDALETGYGKYNP 180
QY 202 YHNOIHAADVTTQVHCFLRGMVHCSEIELLAIIFAAAHDEYHTGTTNSFHQTKSE 261
DQ 181 YHNOIHAADVTTQVHCFLRGMVHCSEIELLAIIFAAAHDEYHTGTTNSFHQTKSE 240
QY 262 CAIYVNDVLENHHSVFLMQDDENNIPTKDEFVELRALVIEMLATDMSCHFQ 321
DQ 241 CAIYVNDVLENHHSVFLMQDDENNIPTKDEFVELRALVIEMLATDMSCHFQ 300
QY 322 QVTKMTALQQLERIDKPKALSLLLHAADI SHPTKQWLVHRSWKALMEEFROGDKAE 381
DQ 301 QVTKMTALQQLERIDKPKALSLLLHAADI SHPTKQWLVHRSWKALMEEFROGDKAE 360
QY 382 LGLPSPCLDRTSTLVAOSQIGFDFIVEPTFSLTVAESVQPLADESKSNQPSFQ 441
DQ 361 LGLPSPCLDRTSTLVAOSQIGFDFIVEPTFSLTVAESVQPLADESKSNQPSFQ 420
QY 442 WRQPSLDVEGDPNPVYFSTRWVKRIQENKQKWKERAAAGITNQMSIDELSPCEEAP 501
DQ 421 WRQPSLDVEGDPNPVYFSTRWVKRIQENKQKWKERAAAGITNQMSIDELSPCEEAP 480
QY 502 PSPAEDHNQNGNLD 516
DQ 481 SSPAEDHNQNGNLD 495

RESULT 4
Q95NB8 PRELIMINARY; PRT; 515 AA.

ID Q95NB8
AC Q95NB8
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Calmodulin-activated cyclic nucleotide phosphodiesterase.
GN PDE1A.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21261952; PubMed=11368912;
RA Clapham J.C., Wilderspin A.F.;
RT "Cloning of dog heart PDE1A, a first detailed characterization at the
molecular level in this species";
RL Gene 268:165-171(2001).
DR EMBL; AF252536; AAK39971.1; JOINED.
DR InterPro; IPR003607; Met_pshphohydro.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF00233; PDEase; 1.
DR PRINTS; PR00387; PD1ESTERASE1.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE_I; 1.

SQ SEQUENCE 515 AA; 59374 MW; BE41DBBBFC1DCC2A CRC64;

Query Match 60.8%; Score 1626.5; DB 6; Length 515;
Best Local Similarity 62.2%; Pred. No. 4.7e-122;
Matches 306; Conservative 90; Mismatches 8; Indels 9; Gaps 1;

QY 1 MANPVQVORSHLQGPILRLRYMVKOLENGEINIEELKKLEYTASLLEAVYIDETRIQILD 60
DQ 1 MDDHVTIRKKHLQRFIFRLCLVQLERGVNVDLKKNIEVAAVLEAVYIDETRIQILD 60
QY 61 TEDEQLERSDAVPSVRDLASTTQARAKGRAEERPKERSIVHVAQAGIFVERMERF 120
DQ 61 TEDELSLQTDSPSEVRDLASTTFRKGMKMKSEKPKERSIVHVAQAGIFVERMERF 120
QY 121 RYTSVGTSTAVLNCKNLDLWCFDVFSLNQAADHALRTIVFELLTRHNLISRFKIP 180
DQ 121 KSYHMGVLVYPEAVITLKDVKDFVFALENGEHLKPMIYELFTRDILIRFKIP 180
QY 181 TVFLMSFLDALETGYGKYNPYHNOIHAADVTTQVHCFLRGMVHCSEIELLAIIFAA 240
DQ 181 VSCLISFAELEVGYSKYKPNVHNLHAADVTTQVHYIMLHTGINHWTLEILAVFAA 240
QY 241 AIHDYHTGTTNSFHQTKSECAIYVNDVLENHHSVFLMQDDENNIPTKDEF 300
DQ 241 AIHDYHTGTTNSFHQTKSECAIYVNDVLENHHSVFLMQDDENNIPTKDEF 300
QY 301 VELRALVIEMLATDMSCHFQVTKMTALQQLERIDKPKALSLLLHAADISHPTKQWLV 360
DQ 301 RDLRLVIEMLATDMSCHFQVTKMTALQQLERIDKPKALSLLLHAADISHPTKQWLV 360
QY 361 HSRWTALMEEFROGDKAEELGPFSPCLDRTSTLVAOSQIGFDFIVEPTFSLTVA 420
DQ 361 HYRTMALMEEFROGDKAEELGPFSPCLDRTSTLVAOSQIGFDFIVEPTFSLTVA 420
QY 421 EKSQVPLADESKSNQPSFQVHRSWKALMEEFROGDKAE-----PNPDVYFSTRWVKRIQ 471
DQ 421 EKIIPLTEEASKTDTSSYGASRRSRNMGKTMDGTSPDYSVLASVLDKSFKNLVDIIQ 480
QY 472 NKQWKERAAAG 483
DQ 481 NKERKELAAAG 492

RESULT 5
Q9COL0 PRELIMINARY; PRT; 529 AA.

ID Q9COL0
AC Q9COL0
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Calmodulin-dependent phosphodiesterase.
GN HSPDE1A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21240211; PubMed=11342109;
RA Michibata H., Yanaka N., Kanoh Y., Okumura K., Omori K.;
RT "Human Ca2+/calmodulin-dependent phosphodiesterase PDE1A: novel splice
variants, their specific expression, genomic organization, and
chromosomal localization".
RL Biochim. Biophys. Acta 1517:278-287(2001).
DR EMBL; AB038224; BAB20055.1; JOINED.
DR EMBL; AB038208; BAB20055.1; JOINED.
DR EMBL; AB038211; BAB20055.1; JOINED.
DR EMBL; AB038213; BAB20055.1; JOINED.
DR EMBL; AB038214; BAB20055.1; JOINED.
DR EMBL; AB038215; BAB20055.1; JOINED.
DR EMBL; AB038216; BAB20055.1; JOINED.
DR EMBL; AB038217; BAB20055.1; JOINED.
DR EMBL; AB038218; BAB20055.1; JOINED.

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DR EMBL; AB038219; BAB20055.1; JOINED.
DR EMBL; AB038220; BAB20055.1; JOINED.
DR EMBL; AB038221; BAB20055.1; JOINED.
DR EMBL; AB038222; BAB20055.1; JOINED.
DR EMBL; AB038223; BAB20055.1; JOINED.
DR EMBL; AB038224; BAB20055.1; JOINED.
DR InterPro; IPR003607; Met_Phsphohydro.
DR SMART; SM00471; Hdc; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
DR SEQUENCE 529 AA; 60649 MW; 39CF97424CC0CE2 CRC64;

Query Match 60.5%; Score 1618; DB 4; Length 529;
Best Local Similarity 59.5%; Pred. No. 2.3e-121;
Matches 311; Conservative 93; Mismatches 95; Indels 24; Gaps 3;

Qy 1 MANPVPQVRSHLQGPILRLRYMVKQLENGEINIEELKKNLEYTASLEAVYIDETRIILD 60
Db 1 MDDHVTIRKHLQRPILRLRYMVKQLENGEINIEELKKNLEYTASLEAVYIDETRIILD 60
Qy 61 TEDELQELRDVAVPSEVRDMLASTFTQQAARAKGRRAEKPFRSIVHVAQAGIFVERMYR 120
Db 61 TEDELSDIQDTSVPSEVRDMLASTFTQQAARAKGRRAEKPFRSIVHVAQAGIFVERMYR 120
Qy 121 RTYTSVGPYTAVALNCLNLDWCFDVSFSLNQAADHDLRTIVFELLTRHNLISRPKIP 180
Db 121 KTHYMGVLAIPAIVITLKDVKWDFVFNALNAGEHSLKPMIYELFTRIDLINEFKIP 180
Qy 181 TVFLMSFLDALETGKGYKNPNHQAADVTQVHCFLRTGMVHCLSEIELLAIIFAA 240
Db 181 VSLITFALEALVGYSKYKNPNHQAADVTQVHCFLRTGMVHCLSEIELLAIIFAA 240
Qy 241 AIHDEHTGTTNSFHQTSKCAIYVNDRSVLNHHISSVFRMQDDENNIFINLKDEF 300
Db 241 AIHDEHTGTTNNFHQTSKCAIYVNDRSVLNHHISSVFRMQDDENNIFINLKDEF 300
Qy 301 VELRALVEMVLATDMSCHFOQVKTMTALQQLERIDKPKALSLLLHAADISHPTKOWLV 360
Db 301 RDLRLNVLVEMVLATDMSCHFOQVKTMTALQQLERIDKPKALSLLLHAADISHPTKOWLV 360
Qy 361 HSRWTKALMEEFROGDKAEGLPSPCLDRTSTLVAQSQIGFIDFIVEPTFSVLTDVA 420
Db 361 HYRTWALMEEFROGDKAEGLPSPCLDRTSTLVAQSQIGFIDFIVEPTFSVLTDVA 420
Qy 421 EKSVOPLADEDSKSNQPSFQWRQPSL-----DVEVGDPNP-----D 457
Db 421 EKSVOPLADEDSKSNQPSFQWRQPSL-----DVEVGDPNP-----D 457
Qy 458 VVSFRSTWVKRIQENKQKWKERAASGITN-QMSIDELSPCEER 499
Db 458 VVSFRSTWVKRIQENKQKWKERAASGITN-QMSIDELSPCEER 499
Qy 481 LKSFKNLVDIIQONKRWKELAAQGESDLHKNSDVLNAAEK 523
Db 481 LKSFKNLVDIIQONKRWKELAAQGESDLHKNSDVLNAAEK 523

RESULT 6
Q9C0L4 PRELIMINARY; PRT; 536 AA.
ID Q9C0L4 PRELIMINARY; PRT; 603 AA.
AC Q8CDV2;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Calmodulin-dependent phosphodiesterase.
GN HSPDEIA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RX MEDLINE=21240211; PubMed=11342109;
RA Michibata H., Yanaka N., Kanoh Y., Okumura K., Omori K.;
RT "Human Ca2+/calmodulin-dependent phosphodiesterase pDEIA: novel splice
RT variants, their specific expression, genomic organization, and
RT chromosomal localization."
RL Biochim. Biophys. Acta 1517:278-287(2001).
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RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium;
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL Nature 420:563-573(2002).";
DR EMBL; AK029531; BAC26499.1; -.
SQ SEQUENCE 603 AA; 68348 MW; 4561AC1AF2FBCF47 CRC64;

Query Match 59.6%; Score 1595; DB 11; Length 603;
Best Local Similarity 60.5%; Pred. No. 1.9e-119;
Matches 310; Conservative 81; Mismatches 81; Indels 40; Gaps 5;

QY 18 RLRYVMVKOLENGEINIEELKKNLKLEYTASILLKLEYIDETROILDTDEQLRSDAVPSEV 77
DB 15 RLRLSVKQLENGEASVVDLKKNLKLEYATVLESVYIDETRRLLDDEQLSDQSDAVPSEV 74
QY 78 RDWLASTFTQOARAKGRRAEKPFRSIVHVAQAGIFVERMFRRTYTSVGPITYSTAVLNC 137
DB 75 RDWLASTFTQGMMLRRSDEKPRKPSIVHVAQAGIFVERMYRTSNMVGLSYPPAVIDA 134
QY 138 LKNLDLWCFDVFSLNQADDDHALRTIVFELLTRHNLISRFKIPITVFLMSFLDALETGYGK 197
DB 135 LKQVDVTFDVFSLNEASGDHALKFIYELLTRYDLISRFKIPISALVSFVEALEVGYSK 194
QY 198 YKNPYHNOIHAADVTQTVHCFLLRTGMVHCLSEIELLAIIFAAAIDHYEHTGTNSFHQ 257
DB 195 HKNPYHNLHMAADVTQTVHYLLYKTGVANWLTELEIFAIIFSAALHDEYHTGTNNFHQ 254
QY 258 TKSECAIYNDRSVLENHHSVFRMQ-DDEMNIFINLTDEFEVLRALVEMVATDM 316
DB 255 TRSDPAIYNDRSVLENHLSAAVRLQDEEMNLVNLSDKDDNREFRTLVIEMVATDM 314
QY 317 SCHFOQVTKMTALQOOLERIDPKKALSLLLHAADISHPTKQWLHRSRTWKALMEFFRQ 376
DB 315 SCHFOQIKAMTKALQOPEAIEPKKALSLMLHTADISHPAKAWDLHRRWTMSLLEEFFRQ 374
QY 377 DKEAELGPFPLCDRTSTLVAQSIGFIDFIVEPTFVSVLTDVAEKSQVPLADEDSKSN 436
DB 375 DREAELGLPFLCDRKSTWVAQSQGFIDFIVEPTFTVLTDMTEKIVSPLIDESSQTGG 434
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DB 435 TQQ-----RRSSLNSINSDAKRGVKSQSGSDGAPINNSVIPDYKSKFATWTEVVQINRE 491
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AC QB8SV6;
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DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE Phosphodiesterase 1c.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
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RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pituitary;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium;
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL Nature 420:563-573(2002).";
DR EMBL; AK029531; BAC26499.1; -.
SQ SEQUENCE 603 AA; 68348 MW; 4561AC1AF2FBCF47 CRC64;

Query Match 59.6%; Score 1595; DB 11; Length 603;
Best Local Similarity 60.5%; Pred. No. 1.9e-119;
Matches 310; Conservative 81; Mismatches 81; Indels 40; Gaps 5;

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DB 255 TRSDPAIYNDRSVLENHLSAAVRLQDEEMNLVNLSDKDDNREFRTLVIEMVATDM 314
QY 317 SCHFOQVTKMTALQOOLERIDPKKALSLLLHAADISHPTKQWLHRSRTWKALMEFFRQ 376
DB 315 SCHFOQIKAMTKALQOPEAIEPKKALSLMLHTADISHPAKAWDLHRRWTMSLLEEFFRQ 374
QY 377 DKEAELGPFPLCDRTSTLVAQSIGFIDFIVEPTFVSVLTDVAEKSQVPLADEDSKSN 436
DB 375 DREAELGLPFLCDRKSTWVAQSQGFIDFIVEPTFTVLTDMTEKIVSPLIDESSQTGG 434
QY 437 QPSFQWRQPSLD-VEVGDPN-----PDVVSFRSTWVKRTOENKQ 474
DB 435 TQQ-----RRSSLNSINSDAKRGVKSQSGSDGAPINNSVIPDYKSKFATWTEVVQINRE 491
QY 475 KWKEAASGITNQMSIDELSCPEEAPPSPAE 506
DB 492 RWRAKV-----PKEAKAKEEE 509

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AC QB8SV6;
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DT 01-JUN-2001 (TremBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
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GN PDE1C.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
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RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
```


[illegible]

RC TISSUE-Testis;
RA Sonnenburg W.K., Yan C., Soderling S., Beavo J.A.;
RT "Identification of a New PDE1A Calmodulin-stimulated Cyclic Nucleotide
Phosphodiesterase Expressed in Mouse Sperm";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF159298; AAF63857.1; -;
DR MGD; MGI:1201792; Pde1a.
DR InterPro; IPR003607; Met_phosphohydro.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF00233; PDEase; 1.
DR PRINTS; PR00387; PD1ESTERASE1.
DR SMART; SM00471; HDC; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
SQ SEQUENCE 456 AA; 52163 MW; EE16EE1FD6837104 CRC64;

Query Match 53.5%; Score 1431.5; DB 11; Length 456;
Best Local Similarity 61.0%; Pred. No. 1.8e-106;
Matches 275; Conservative 74; Mismatches 79; Indels 23; Gaps 2;

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QY 116 ERMERTYTSVGPYSTAVLNLCKNLKLDLWCFDVSINOADDHALRTIVFELLTRHNLIS 175
D 175
Db 64 ERMVKNYHMYGLTYPAAVIIVTLKEVDKWSFDVFNALNEASGEHSLKFMIEYELTRYDLIN 123
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Job time : 74 secs

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OM nucleic - nucleic search, using sw model

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Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

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Listing first 45 summaries

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- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

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and is derived by analysis of the total score distribution.

SUMMARIES

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6	2110	68.3	2265	9	HSU56976	HSU56976 Human calmo
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ALIGNMENTS

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LOCUS AX139124
DEFINITION Sequence 2 from Patent EP1085092.
ACCESSION AX139124
VERSION AX139124.1 GI:14274800
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Homidae; Homo.
REFERENCE
AUTHORS Fldock,M.D.
TITLE Phosphodiesterase enzymes
JOURNAL Patent: EP 1085092-A 2 21-MAR-2001;

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LOCUS
DEFINITION
AJ401609 Homo sapiens (human)
ACCESSION
AJ401609.1 GI:16151612
VERSION
3'5' cyclic nucleotide phosphodiesterase 1B2; alternative splicing;
KEYWORDS
PDE1B2 gene.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Fidock, M., Miller, M. and Lanfear, J.
AUTHORS
TITLE
Isolation and differential tissue distribution of two human cDNAs encoding PDE1 splice variants
JOURNAL
Cell. Signal. 14 (1), 53-60 (2002)
MEDLINE
21614508
PUBMED
11747989
REFERENCE
2 (bases 1 to 2985)
AUTHORS
Fidock, M.D.
TITLE
Direct Submission
JOURNAL
Submitted (18-AUG-2000) Fidock M.D., Discovery Biology, Pfizer
Global Research and Development, Ransgate Road, Sandwich, Kent CT13
9NU, UNITED KINGDOM
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Qy	955	CTCTGTTTCCGATTGATCAGGATGATGAGATGAACATTTTCATCAACCTCACCAAGGA	1014		2035	TCGCCCATCTTTTGGCTTCCAGTTCCTTAAGCAATACATTTTGGGGTTCCTTCAGCC	2094
Db	1060	CTCTGTTTCCGATTGATCAGGATGATGAGATGAACATTTTCATCAACCTCACCAAGGA	1119		2140	TCGCCCATCTTTTGGCTTCCAGTTCCTTAAGCAATACATTTTGGGGTTCCTTCAGCC	2199
Qy	1015	TGAGTTTGTAGAACTCCGAGCCCTGGTTCATGAGATGTTGGCCACAGATGCTCCTG	1074		2095	CCACGCCACAGATTTAGCTGGCAGGTCTGGGTGCCCTTTTCTCCCTGGGAAGGGCTG	2154
Db	1120	TGAGTTTGTAGAACTCCGAGCCCTGGTTCATGAGATGTTGGCCACAGATGCTCCTG	1179		2200	CCACGCCACAGATTTAGCTGGCAGGTCTGGGTGCCCTTTTCTCCCTGGGAAGGGCTG	2259
Qy	1075	CGATTTCCAGCAAGTGAAGACCCATGAAGACAGCTTTCGAACAGCTGGAGAGATTGACAA	1134		2155	GAATAGGATPAGAAAGCTGGGGTTTTCAGAGCCCTATGTGTGGGAGGAGTGGATTCC	2214
Db	1180	CGATTTCCAGCAAGTGAAGACCCATGAAGACAGCTTTCGAACAGCTGGAGAGATTGACAA	1239		2260	GAATAGGATPAGAAAGCTGGGGTTTTCAGAGCCCTATGTGTGGGAGGAGTGGATTCC	2319
Qy	1135	GCCCAAGGCCCTGCTCTACTGCTCCATGCTGTGACATCAGCCACCCCAACCAAGCAGTG	1194		2215	TTACGGGCTATGTACTCTTTCTAGGATCTGGGAATGGGTGGAGAGACATCTCTTCAC	2274
Db	1240	GCCCAAGGCCCTGCTCTACTGCTCCATGCTGTGACATCAGCCACCCCAACCAAGCAGTG	1299		2320	TTACGGGCTATGTACTCTTTCTAGGATCTGGGAATGGGTGGAGAGACATCTCTTCAC	2379
Qy	1195	GTTGTGTCACAGCCGTTGGACCAAGCCCTCATGGAGGAATTTCTCCGTCAGGGTGACAA	1254		2275	CCAGAAATTTGCGTGTCTTTCAGCCCATCTCCAGCCCTGATCCTCTGAATCTTCCCTCC	2334
Db	1300	GTTGTGTCACAGCCGTTGGACCAAGCCCTCATGGAGGAATTTCTCCGTCAGGGTGACAA	1359		2380	CCAGAAATTTGCGTGTCTTTCAGCCCATCTCCAGCCCTGATCCTCTGAATCTTCCCTCC	2439
Qy	1255	GGAGGACAGATTGGGCTGCCCTTTTCTCCACTCTGTGACCCGACATTCACACTCTAGTGGC	1314		2335	CTTCTGTATACAGTACTGGGGCAAAAGAGCCATTGTGACCAGGGGCTGCGGGAGGCT	2394
Db	1360	GGAGGACAGATTGGGCTGCCCTTTTCTCCACTCTGTGACCCGACATTCACACTCTAGTGGC	1419		2440	CTTCTGTATACAGTACTGGGGCAAAAGAGCCATTGTGACCAGGGGCTGCGGGAGGCT	2499
Qy	1315	ACAGTCTCAGATAGGTTTCATGACATTCATTTGGAGCCACATTCCTGTGCTGACTGA	1374		2395	TTCTCTGGGACCTTCTTGGGACTGGTCTGGGGCCCTGGGGCTTGTGCGCTGCGCTGAGTC	2454
Db	1420	ACAGTCTCAGATAGGTTTCATGACATTCATTTGGAGCCACATTCCTGTGCTGACTGA	1479		2500	TTCTCTGGGACCTTCTTGGGACTGGTCTGGGGCCCTGGGGCTTGTGCGCTGCGCTGAGTC	2559
Qy	1375	CGTGGCAGAGAGAGTGTTCAGCCCTTGGCGGATGAGGACTCCAAGTCTAAAAACAGCC	1434		2455	CGGAGCCCTTTTGGCTTCTCTCCCTGGGGCTGGGAGGCTCCATCCGACCAATGCT	2514
Db	1480	CGTGGCAGAGAGAGTGTTCAGCCCTTGGCGGATGAGGACTCCAAGTCTAAAAACAGCC	1539		2560	CGGAGCCCTTTTGGCTTCTCTCCCTGGGGCTGGGAGGCTCCATCCGACCAATGCT	2619
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Db	1540	CAGCTTTTCACTGGCGCAGCCCTCTCTGATGTGAAGTGGAGAGCCCAACCTCTGATGT	1599		2620	GTAAAGTGTCTTTGAGGATCTCCCAAGCAAGACCTTCAGAAATGTATGACACACAGCTGG	2679
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					2800	TGAGACAAAGTGAAGGGTGTCTGGTGAAGGACAGATGGACAAAGGGCTCAGGCTCTGCTG	2859

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QY 355 GGACTGGCTGCCCTCCACCTTCACCCAGCAGCCCGGGCCAAAGGCCCGCAGCAGAGA 414
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RESULT 7
MUSPDE1B1
LOCUS Mus musculus calmodulin-dependent phosphodiesterase (PDE1B1) mRNA,
DEFINITION complete cds.
ACCESSION L01695
VERSION L01695.1 GI:200269

http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html.

Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L. L.,
Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojebokan, I., Rolfe, M.,
Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shim, C.,
Shoemaker, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A.,
Stanton, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A.,
Tantisi, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Teifrod, B.,
Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D.,
Vinson, R., Wall, R., Wang, S., Ward-Moore, S., Warren, R.,
Washington, C., Watlington, S., Williams, G., Williamson, A.,
Worley, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y. F., Zhou, J.,
Zorilla, S., Kucherlapati, R. and Gibbs, R.

Direct Submission
Unpublished
2 (bases 1 to 180971)
Worley, K.C.
Direct Submission
Submitted (27-AUG-2000) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 180971)
Worley, K.C.
Direct Submission
Submitted (01-JAN-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 180971)
Worley, K.C.
Direct Submission
Submitted (15-MAR-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
5 (bases 1 to 180971)
Worley, K.C.
Direct Submission
Submitted (27-APR-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jan 2001 this sequence version replaced g1:11968205.
INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email
gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the
entire insert of this clone. Overlapping regions of clones are only
sequenced and submitted once, so the sequence for the remainder of
the insert may be found in the record for the adjacent clones.
Overlapping clones are noted at the beginning and end of the
Features listing.

ANNOTATION OF FEATURES:
STSs are identified using ePCR (Genome Res. 7:541-550) searches
of a local database that includes entries from dbSTS, GDB, and
local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green,
unpublished.) for Human and Mouse sequences.
Genes and Region of sequence similarity are identified by BLAST
(Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the
EST and cDNA sequences. Genes demonstrate at least two exons
flanked by consensus splice sites that maintained sequence
continuity across the splice junctions. Sequences that are not
identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum
standard of double strand coverage with a minimum of 2 clones and 2
reads with no ambiguities or 2 chemistries with a minimum of 2
clones and 3 reads with no ambiguities. If the sequence quality for
a region does not meet this standard, it will be indicated in the
annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality
standards - estimated error rate less than 1 per 10,000 bases.
Reports of lowest quality individual bases and measures of base
quality are listed below. Description of the metrics can be found
at URL:

Position	Original+Context	Edited+Context
415	aaagtgggg(n)agctgccag	aaagtgggg(g)agctgccag
5301	tgtctcaaaa(n)aaataataa	tgtctcaaaa(t)aaataataa
5337	tgaagatat(n)catatataa	tgaagatat(t)catatataa
5355	atataatat(n)ttttttgtt	atataatat(c)ttttttgtt
5381	acagagttta(n)ttttgtgcc	acagagttta(c)ttttgtgcc
5382	cgaggtttan(n)ttttgtgcc	cgaggtttac(t)ttttgtgcc
5382	gggttcaag(n)attttctgc	gggttcaag(a)attttctgc
5393	agcnaattct(n)ctgctcagc	agcnaattct(t)ctgctcagc
5399	ctcagctctc(n)gagtagggt	ctcagctctc(t)gagtagggt
5374	attttagta(n)tggtatgct	attttagta(g)tggtatgct
6033	ctgacactca(n)tggtatgct	ctgacactca(g)tggtatgct
6084	actcaagtc(n)tggtatgct	actcaagtc(t)tggtatgct
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DB 151673 TTAATGTTCCGGCAGCAGACTGGGGAACCTTCAGGCTCCAGTGTCCATCCATCC 151732
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ACCESSION AR016548
VERSION AR016548.1 GI:3972825
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SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1844)
AUTHORS Beavo,J.A., Bentley,J.Kelley., Charbonneau,H. and Sonnenburg,W.K.
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DEFINITION complete cds.
ACCESSION M94867
VERSION 1.1
KEYWORDS 63 kDa calmodulin-stimulated phosphodiesterase.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 1842)
Bentley, J.K., Kadlec, A., Sherbert, C.H., Seger, D., and Beavo, J.A.
Schneiberg, W.K., Charbonneau, H., Novack, J.P., and Beavo, J.A.
Molecular cloning of cDNA encoding a '63'-kDa calmodulin-stimulated
phosphodiesterase from bovine brain
J. Biol. Chem. 267 (26), 18676-18682 (1992)
92406781
2 (bases 1 to 1842)
Beavo, J.A.
Direct Submission
Submitted (20-JUL-1992) Joe A. Beavo, Department of Pharmacology,
SU-30, University of Washington, Seattle, WA 98195, USA
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 QY 1675 CTGGGCGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1734
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 Db 1837 CAAGG 1841

Search completed: August 10, 2003, 20:52:41
 Job time : 10916 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 10, 2003, 16:42:40 ; Search time 764 Seconds
(without alignments)
10921.417 Million cell updates/sec

Title: US-09-663-481-2
Perfect score: 3091
Sequence: 1 gtgaccacgcgtccggga.....aaaaaaaaaaaaaaaaaaaaa 3091

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3091	100.0	3091	22	Human cyclic nucle
2	2903.6	93.9	3054	20	Human brain cell s
3	2106.8	68.2	2265	20	Human RPMI 8392 ce
4	1347.6	43.6	1844	16	Cyclic-GMP stimula
5	1347.6	43.6	1844	18	Bovine brain 63 kD
6	1347.6	43.6	1844	18	cdna for 63 kD cal
7	1347.6	43.6	1844	19	Bovine brain Ca2+/
8	1347.6	43.6	1844	19	63 kDa Cam-PDE DNA

9	1347.6	43.6	1844	19	AAV36148	Bovine Cam-PDE CDN
10	1347.6	43.6	1844	21	AAZ90372	Bovine brain 63 kD
11	1347.6	43.6	1844	25	ABX78849	Bovine brain cDNA
12	1342.8	43.4	1844	13	AAQ30175	63 kD Cam PDE CDNA
13	598	19.3	2693	16	AAQ83981	Cyclic-GMP stimula
14	598	19.3	2693	18	AAAT67202	Human brain 61 kDa
15	598	19.3	2693	18	AAAT51116	Hippocampus calcu
16	598	19.3	2693	19	AAV54765	Human 61 kDa Cam-P
17	598	19.3	2693	19	AAV48208	Human Ca2+/calmodu
18	598	19.3	2693	19	AAV36160	cDNA encoding a hu
19	598	19.3	2693	21	AAZ90384	Human 61 kD Cam-PD
20	598	19.3	2693	25	ABX78861	Human cDNA encodin
21	593.2	19.2	2693	13	AAQ30187	cDNA insert of pca
22	579.8	18.8	2656	13	AAQ30172	Bovine lung 59 kD
23	579.8	18.8	2656	16	AAQ83964	Cyclic-GMP stimula
24	579.8	18.8	2656	18	AAAT67199	Bovine lung 59 kDa
25	579.8	18.8	2656	18	AAAT51091	Coding sequence fo
26	579.8	18.8	2656	19	AAV48191	Bovine lung Ca2+/c
27	579.8	18.8	2656	19	AAV54748	59 kDa Cam-PDE CDN
28	579.8	18.8	2656	19	AAV36143	Bovine Cam-PDE CDN
29	579.8	18.8	2656	21	AAZ90367	Bovine lung 59 kD
30	579.8	18.8	2656	25	ABX78844	Bovine heart cDNA
31	578.8	18.7	1625	16	AAQ83980	Cyclic-GMP stimula
32	578.8	18.7	1625	18	AAAT67201	Human brain 61 kDa
33	578.8	18.7	1625	18	AAAT51115	Hippocampus calcu
34	578.8	18.7	1625	19	AAV54764	Human 61 kDa Cam-P
35	578.8	18.7	1625	19	AAV48207	Human Ca2+/calmodu
36	578.8	18.7	1625	19	AAV36159	cDNA encoding a hu
37	578.8	18.7	1625	21	AAZ90383	Human 61 kD Cam-PD
38	578.8	18.7	1625	25	ABX78860	Human cDNA encodin
39	578.8	18.7	2008	22	AAAD14515	Human phospholipase
40	578.8	18.7	2008	22	AAAD14525	Human phospholipase
41	578.8	18.7	2008	22	AAAF84074	Human 3', 5' cycli
42	578.8	18.7	2008	22	AAAF84084	Human 3', 5' cycli
43	577.2	18.7	1763	23	AAAT5915	DNA encoding novel
44	574	18.6	1625	13	AAQ30186	cDNA insert of pHc
45	559.6	18.1	2291	16	AAQ83957	Cyclic-GMP stimula

ALIGNMENTS

RESULT 1
AAAF62301
ID AAF62301 standard; cDNA; 3091 BP.
XX
AC AAF62301;
XX
DT 06-JUN-2001 (first entry)
XX
DE Human cyclic nucleic acid phosphodiesterase PDE1B2 coding sequence.
XX
KW Human; cyclic nucleic acid phosphodiesterase; PDE1B2; sexual dysfunction;
KW cardiovascular disease; gastrointestinal disorder; spleen; ss.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 122..1672
FT FT /*tag= a
FT FT /product= "PDE1B2"
XX
PN EP1085092-Al.
XX
PD 21-MAR-2001.
XX
PF 14-SEP-2000; 2000EP-0307982.
XX
PR 17-SEP-1999; 99GB-0022125.
XX
PA (PFIZ) PFIZER LTD.
XX (PFIZ) PFIZER INC.

QY 1801 AAATGCCAGAGATTTGGGTTGGGAAAGGGCCCTCCCTCCCTGACACCCACTGGGGTG 1860
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RESULT 2

AAH57561

ID AAH57561 standard; cDNA; 3054 BP.

XX AAH57561;

AC AC

XX XX

DT 10-SEP-2001 (first entry)

XX Human brain cell specific cDNA sequence SEQ ID NO:401.

DE Human; tissue specific; diagnosis; brain; heart; skeletal muscle;

KW lung; liver; uterus; ovary; stomach; intestine; kidney; pancreas; ss;

KW metabolic disease; developmental disease; cytostatic; immunomodulatory;

KW neuroprotective; gene therapy; cancer; immunopathology; neuropathology.

OS Homo sapiens.

XX WO200132927-A2.

PN 10-MAY-2001.

XX 02-NOV-2000; 2000WO-US30396.

PF 04-NOV-1999; 99US-0163508.

XX (INCY-) INCYTE GENOMICS INC.

PA Sornasse T, Seilhamer JJ, Watson GA;

PI WPI; 2001-291057/30.

XX New cell and tissue specific polynucleotides useful for diagnosis,

PT prognosis or monitoring of treatments for disorders where the gene is

PT associated with a cancer, immunopathology or neuropathology -

XX Claim 1; Page 315; 327pp; English.

XX AAH57161 to AAH57576 represent cell and tissue specific polynucleotide

CC sequences (I). (I) can have cytostatic, immunomodulatory and

CC neuroprotective activities, and can be used in gene therapy. (I) and

CC proteins (II) encoded by then are used in high throughput screening

CC assays to select DNA molecules, RNA molecules, peptide nucleic acids,

CC mimetics, peptides, proteins, agonists, antagonists, antibodies or

CC their fragments, immunoglobulins, inhibitors, drug compounds and

CC pharmaceutical agents. Expression of (I) in a sample indicates the

CC differentiation of embryonic stem cells into a tissue selected from

CC brain, heart, kidney, liver, lung, skeletal muscle or pancreatic

CC tissues. (I) and (II) are used to produce an expression profile that

CC defines a metabolic or developmental process, treatment, condition,

CC disease or disorder. The gene profile can be used for diagnosis,

CC prognosis or monitoring of treatments and for investigating a

CC predisposition to a disorder where the gene is associated with a

CC cancer, immunopathology or neuropathology.

XX Sequence 3054 BP; 671 A; 884 C; 830 G; 669 T; 0 other;

SQ Query Match 93.9%; Score 2903.6; DB 22; Length 3054;

Best Local Similarity 99.9%; Pred. No. 0; Matches 2906; Conservative 0; Mismatches 4; Indels 0; Gaps 0;			
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Db	445	GTTCCGGAGAACATACACCTCTGGGCCCACTTACTCTACTGCGGTCTCAACTGTCT	504
QY	535	CAGAACCTGGATCTGGTGTGATGTCCTTTCTTGAACACAGGACAGATGACCA	594
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QY	895	CAAGTCAGAAATGTGCCATCGTGTACATGATGCTTTCAGTGTGAGAAATCACCACATCAG	954
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QY	955	CTCTGTTTTCCGATTTGATGAGGATGATGAGATGAACTTTTCACTCAACCTCAGCCAGGA	1014
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DB 2425 CGGAGCCCTTGGCCCTTCCCTGCTCCCTGGGCTGGGAGGCTCCATCGGACCAATGTCT 2484
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```

RESULT 3

AAAX26288

ID AAX26288 standard; cdna; 2265 BP.

XX AC AAX26288;

XX DT 26-MAY-1999 (first entry)

XX DE Human RPMI 8392 cell phosphodiesterase, PDE1B1 encoding CDNA.

XX KW Antisense oligodeoxynucleotide; phosphodiesterase; PDE1B1; enzyme; PDE;

XX KW cell death; apoptosis; cancer; Ca2+-calmodulin; lymphoblastoid; RNase H;

XX KW RPMI 8392; RNA degradation; cAMP; immunoproliferative disorder; breast;

XX KW immune dysfunction; acute lympholytic leukemia; prostate; human; ss.

XX OS Homo sapiens.

XX PN US5885834-A.

XX

```
PD 23-MAR-1999.
XX 30-SEP-1997; 97US-0940332.
XX 30-SEP-1996; 96US-0027207.
XX 30-SEP-1997; 97US-0940332.
XX (EPST/) EPSTEIN P M.
XX Epstein PM;
XX WPI; 1999-228548/19.
XX P-PSDB; AAW95110.
XX Antisense oligodeoxynucleotides specific for mRNA encoding
XX phosphodiesterase PDE1B1 enzymes and method for using them to induce
XX apoptosis of cells - useful in the treatment of immunoproliferative
XX disorders and immune dysfunctions
XX PS Disclosure: Fig 8A-D; 35pp; English.
XX
XX The invention relates to antisense oligodeoxynucleotides (AS-ODN) which
XX will bind to mRNA encoding phosphodiesterase PDE1B1 enzymes and their use
XX in inducing programmed cell death (apoptosis) in cancer cells. PDE1 is a
XX Ca2+-calmodulin dependent phosphodiesterase found in cytosolic extracts
XX of human lymphoblastoid cell line, RPMI 8392. The method in which
XX programmed cell death is induced in cancer cells comprises: (1)
XX identifying the phosphodiesterase enzyme PDE1B1 in a cell line containing
XX the cancer cells; (2) synthesising an AS-ODN inhibitor which will bind to
XX mRNA encoding PDE1B1; and (3) applying the AS-ODN to the cell line to
XX inhibit the enzymatic activity of the PDE1B1 and induce apoptosis in the
XX cells. The AS-ODNs inhibit the expression of a protein by two mechanisms:
XX (i) by degradation of RNA by the ubiquitous enzyme RNase H, which
XX selectively cleaves the RNA of DNA-RNA heteroduplexes; and (ii) the
XX arrest of translation initiation caused by AS-ODN hybridization to the 5'
XX un-translated region or the translation initiation site on the mRNA.
XX Inhibition of phosphodiesterase (PDE) enzyme expression results in
XX elevated levels of cAMP in the cells due to PDE1B1 being involved in the
XX metabolism of cAMP. The elevated cAMP levels result in apoptosis by
XX inhibition of DNA synthesis. The method and AS-ODN are useful in inducing
XX cAMP stimulated apoptosis and in the treatment of immunoproliferative
XX disorders and immune dysfunctions such as acute lympholytic leukemia,
XX breast and prostate cancer. The present sequence represents a cDNA
XX encoding a human RPMI 8392 cell PDE1B1.
XX
XX Sequence 2265 BP; 507 A; 628 C; 627 G; 500 T; 3 other;
Query Match 68.2%; Score 2106.8; DB 20; Length 2265;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2111; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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DB 148 GCTGCGCTACATGGTGAAGCAGCTTGTGAGAGTGGGAGATGAACATTTGAGGAGCTGAAGAA 207
QY 235 AAATCTGGAGTACACAGCTTCTCTGCTGGAAGCCGCTTACATAGATGAGACACGCAAT 294
DB 208 AAATCTGGAGTACACAGCTTCTCTGCTGGAAGCCGCTTACATAGATGAGACACGCAAT 267
QY 295 CTTGACACGAGGAGGAGCTGCGAGCTGCGGCTCAGATGCGGCTTCCGAGGTGGG 354
DB 268 CTTGACACGAGGAGGAGCTGCGAGCTGCGGCTCAGATGCGGCTTCCGAGGTGGG 327
QY 355 GGACTGCGCTGCGCTCCACCTTCCACCCAGCAGCCGCGGCAAGCCGCCGAGCAGAGA 414
DB 328 GGACTGCGCTGCGCTCCACCTTCCACCCAGCAGCCGCGGCAAGCCGCCGAGCAGAGA 387
QY 415 GAAGCCCAAGTTCGGAAGCATTTGTCAGCTGTCAGGCTGGGATCTTCGTGGAACGAT 474
DB 388 GAAGCCCAAGTTCGGAAGCATTTGTCAGCTGTCAGGCTGGGATCTTCGTGGAACGAT 447
QY 475 GTTCCGAGAGAACATACCTCTGTGGGCCCACTTACTCTACTCGGTTCTCAACTGTCT 534
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PD 14-FEB-1995.
XX PF 20-APR-1992; 92US-0872644.
XX PR 19-APR-1991; 91US-0688356.
XX PR 20-APR-1992; 92US-0872644.
XX PA (UNIW) UNIV WASHINGTON.
XX PI Beavo JA, Charbonneau H, Sonnenburg WK;
XX DR WPI; 1995-090205/12.
XX DR P-P5DB; AAR69720.
XX PT New nucleic acid encoding cyclic-GMP stimulated nucleotide
PT phospho-di:esterase - and related vectors and transformed cells,
PT useful for screening cpds. for phospho-di:esterase modulating
PT activity
XX PS Claim 3; Columns 55-60; 69pp; English.
XX CC AA083969 encodes AAR69720 the bovine brain cyclic-GMP stimulated
CC nucleotide phospho-diesterase (Cam_PDE) clone pl2.3a. Eukaryotic cells
CC that express Cam_PDE can be used to screen cpds. for the ability to
CC modulate Cam_PDE activity. Cam_PDEs are involved in regulating
CC the transmission of information from hormones, neurotransmitters
CC or other systems that use cyclic nucleotides as messengers.
CC Antibodies raised against Cam_PDE can be used for enzyme purifcn.,
CC or determination.
XX CC (Updated on 25-MAR-2003 to correct PF field.)
XX SQ Sequence 1844 BP; 417 A; 551 C; 514 G; 362 T; 0 other;
Query Match 43.6%; Score 1347.6; DB 16; Length 1844;
Best Local Similarity 90.6%; Pred. No. 0;
Matches 1473; Conservative 0; Mismatches 144; Indels 9; Gaps 3;
QY 175 GCTGGCTACATGTTGAAGCAGTGGAGAAATGGGAGATAAACATTGAGGAGCTGAAGAA 234
DB 224 GCTGGCTACATGTTGAAGCAGTGGAGAAATGGGAGATAAACATTGAGGAGCTGAAGAA 283
QY 235 AAATCGAGTACAGAGCTTCTGCTGGAAGCCCTACATAGATGAGACACGGCAAT 294
DB 284 AAACCTGGAGTACAGAGCTTCTGCTGGAGCCGCTATATAGATGAGACTCGGCAAT 343
QY 295 CTTGACACGGAGGAGCTGACAGAGCTGCGGTACAGTCCGTCGCTCGAGGTGCG 354
DB 344 CTTGACACGGAGGAGTACAGAGCTGCGGTACAGTCCGTCGCTCGAGGTGCG 403
QY 355 GGACTGGCTGCTCCACCTTACCCAGCAGCCCGGCGCAAGGCGCCGCGAGCAGAGGA 414
DB 404 GGACTGGCTGCTCCACCTTACCCAGCAGCCCGGCGCAAGGCGCCGCGAG--CGAAGA 460
QY 415 GAAGCCCAAGTTCGAAGCATTTGCGAGCTGTGCGAGCTGGGATCTTCGTGGAAACGGAT 474
DB 461 GAAGCCCAAGTTCGGAGCATCGTGCACGCGGTGCGAGCTGGGATCTTCGTGGAGCGGAT 520
QY 475 GTTCGGAGAAATACATCTGTGGGCGCCCACTTACTCTACTCGGTCTCACTGCTCT 534
DB 521 GTTCGGAGAAACGTACACCTCTGTGGGCGCCCACTTACTCTACTCGGTCTCACTGCTCT 580
QY 535 CAAGAATCTGGATCTCTGGT 594
DB 581 CAAGAATCTGGACCTTGGT 640
QY 595 TGCCCTGAGGACCATTTTGT 654
DB 641 CGCCCTGAGGACCATTTTGT 700
QY 655 GATTCCTGATGTTTGT 714
DB 701 GATTCCTGATGTTTGT 760
QY 715 CAAGAATCTTTACACAAACCAGATCCACGCGAGCCGATGTTACCCAGACAGTCCATTCGTT 774
DB 761 CAAGAATCTTTACACAAACCAGATCCACGCGAGTCCAGCTACCCAGACGGTCCATTCGTT 820
QY 775 CTTGCTCCGACAGGGATGGTGCATGCTGCTGCGAGATTTGAGCTCCCTGGCCATCATCTT 834
DB 821 CTTGCTCCGACAGGGATGGTGCATGCTGCTGCGAGATTTGAGCTCCCTGGCCATCATCTT 880
QY 835 TGCTGACGATTCATCATGATTTAGCACACAGGGCACTACCAACAGCTTTCCACATCCAGAC 894
DB 881 TGCTGACGATTCATCATGATTTAGCACACAGGGCACTACCAACAGCTTTCCACATCCAGAC 940
QY 895 CAAGTCAGATGTGCCATCGTGTACAATGATGCTGCTGCTGCGAGATTTGAGCTCCCTGG 954
DB 941 CAATTCGGAATGCGCCATCTCTACACAGACCGCTGCTGCTGCGAGATTTGAGCTCCCTGG 1000
QY 955 CTCGTTTTTCCGATTTGATGCGAGGATGATGATGATGATGATGATGATGATGATGATG 1014
DB 1001 CTCGTTTTTCCGATTTGATGCGAGGATGATGATGATGATGATGATGATGATGATGATG 1060
QY 1015 TGAGTTTCTAGAACTCCGAGCCCTGCTCATTTGAGATGTTGTTGGCCACAGACATTCCTGT 1074
DB 1061 TGAGTTTCTAGAGCTGCGGGCTCTGCTCATTTGAGATGTTGTTGGCCACAGACATTCCTGT 1120
QY 1075 CCATTTCAGCAAGTGAAGACCATGAAGACAGCTTTGCAACAGCTGGAGAGATTTGACAA 1134
DB 1121 CCATTTCAGCAAGTGAAGTCCATCAAGACAGCTTTGCAACAGCTGGAGAGATTTGACAA 1180
QY 1135 GCGCAAGCCCTGCTCTACTGCTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1194
DB 1181 GTCCAAAGCCCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1240
QY 1195 GTTGTGTCACAGCGCTTGGACCAAGCCCTCATGAGGAATTTCTTCCTGAGGTGACAA 1254
DB 1241 GTCGTTTCAAGCCCTGCTGACCAAGCCCTCATGAGGAATTTCTTCCTGAGGTGACAA 1300
QY 1255 GGAGCGAGATTTGGCCCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1314
DB 1301 GGAGCTCAGCTGGCCCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1360
QY 1315 ACAGTCTCAGATAGGGTTTCATCGACTTTCATTTGTTGGAGCCCATTTCTCTGCTGCTG 1374
DB 1361 GCAGTCCAGATTTGGTTTTCATCGACTTTCATTTGTTGGAGCCCATTTCTCTGCTGCT 1420
QY 1375 CTTGCGCAGAGAGAGTTCAGCCCTGCGGATCAGGACTCCAAAGTCTTAAACACCGCC 1434
DB 1421 TGTGCTGAGAAAGAGTGTCCAGCCCTGCGGAGCCAGCTGGAAGTCTTAAACACCGCC 1480
QY 1435 CAGCTTTTCAGTGGCCCGAGCCCTCTCTGATGTTGGAAGTGGAGAGCCCAACCCCTGT 1494
DB 1481 CAGCTTTTCAGTGGCCCGAGCCCTCTCTGATGTTGGAAGTGGAGAGCCCAACCCCTGT 1540
QY 1495 GGTACGCTTCTGTTCCACTGCGGTCAAGCCATTCAGGAGATTAAGCAGAAATGGAAGA 1554
DB 1541 GGTACGCTTCTGTTCCACTGCGGTCAAGCCATTCAGGAGATTAAGCAGAAATGGAAGA 1600
QY 1555 ACGGCAGCAAGTGGCATCACCAACAGATGTCATTTGACGAGCTTCCCTCTGTTGAAGA 1614
DB 1601 ACGGCGGGAGGCGCATCACCAACAGATGTCATTTGACGAGCTTCCCTCTGTTGAAGA 1660
QY 1615 AGAGCCCGCCCATCCCTGCGGAAGATGAACACAAACAGAAATGGAAATTCGGATAGCC 1674
DB 1661 AGAGCCCGCCCATCCCTGCGGAAGATGAACACAAACAGAAATGGAAATTCGGATAGCC 1719
QY 1675 CTGGGCTGGCCAGGCTTCTTATGAGTCCAAAGTGTGTTGATGCTCATCAGCAACCAT 1734
DB 1720 --GGGCGCTGGCCAGGCTTCTTATGAGTCCAAAGTGTGTTGATGCTCATCAGCAACCAT 1777
QY 1735 CAGGACTGCTCCCGCATCTGCTCAAGGAGCGTG--GTCGTGGAAGAAACACCCAC 1791
DB 1778 CGGAGCTGGCTCCCGCATCTGCTCCGAGGCGGAATGGATGTCAGGAACAGAAACCCAC 1837
QY 1792 CTGAAG 1797

[illegible]

QY 1435 CAGCTTTTCAGTGGCCAGCCCTCTCTGTGATCTGGAAGTGGAGACCCCAACCCCTGTATG 1494
Db 1481 CAGCTTCCAGTGGCGCAGCCCTCTCTGTGATGTAAGTGGAGACCCCAACCCCTGTATG 1540
QY 1495 GGTACGTTTCTGTTCCAGCTGGTCAAGCGATTCAGGAGATAGCAGAAATGGAAGGA 1554
Db 1541 GGTACGTTTCTGTTCCAGCTGGTCAAGCGATTCAGGAGATAGCAGAAATGGAAGGA 1600
QY 1555 AGCGGACGAAGTGGCATCACCAACAGATGTCATTCAGGAGTGTCCCTCTGTGAAGA 1614
Db 1601 AGCGGCGGAGGCGCATCACCAACAGATGTCATTCAGGAGTGTCCCTCTGTGAAGA 1660
QY 1615 AGAGGCCCCCTATCCCTGCGGAAGATGAACACACAGAAATGGGAATCTGGATAGCC 1674
Db 1661 AGAGGCCCCCTATCCCTGCGGAAGATGAACACACAGAAATGGGAATCTGGATAGC- 1719
QY 1675 CTGGGCTGGCCAGGTTCTTATTCAGTCCAAAGTGTGTGATGTCATCAGCAATCCAT 1734
Db 1720 --GGGGCTGGCCAGGTTCTTATTCAGTCCAAAGTGTGTGATGTCATCAGCAATCCAT 1777
QY 1735 CAGGACTGGCTCCCTCCATCTGCTCAAGGGAGCGTG---GTCGTGGAAGAAACACCCAC 1791
Db 1778 CGGGACTGGCTCCCTCCATCTGCTCGAGGGCGAATGGATGTCAGGAACAGAAACCCAC 1837
QY 1792 CTGAAG 1797
Db 1838 CCGAAG 1843.

RESULT 6

ID AAT51105
AC AAT51105 standard; cDNA; 1844 BP.
AC AAT51105;
XX 25-MAR-2003 (updated)
DT 17-MAR-1997 (first entry)
XX
DE cDNA for 63 kD calcium/calmodulin dependent phosphodiesterase.
XX
KW Cyclic GMP stimulated phosphodiesterase; cGS-PDE; bovine; brain; cAMP;
KW adrenal gland; transmembrane signal; extracellular hormone; antibody;
KW neurotransmitter; cGMP; calcium/calmodulin dependent phosphodiesterase;
KW Cam-PDE; ss.
XX
OS Bos taurus.
XX
FH Key Location/Qualifiers
FT CDS 114..1718
FT /tag= a
FT /product= calcium/calmodulin dependent phosphodiesterase
XX
XX US5580771-A.
XX
PD 03-DEC-1996.
XX
XX 29-AUG-1994; 94US-0297494.
XX
PR 20-APR-1992; 92US-0872644.
PR 19-APR-1991; 91US-0688356.
PR 29-AUG-1994; 94US-0297494.
XX
XX (UNIW) UNIV WASHINGTON.
XX
XX Beavo JA, Charbonneau H, Sonnenburg WK;
XX
XX WPI; 1997-035573/03.
DR P-PSDB; AAW11251.
XX
XX DNA encoding cGMP-stimulated phosphodiesterase - for prodn. of
PT recombinant enzyme
XX
XX Example 3; Column 53-58; 68pp; English.

XX This sequence represents the coding sequence for the 63 kD
CC calcium/calmodulin dependent phosphodiesterase (Cam-PDE) clone p12.3a
CC isolated from bovine brain. The cyclic nucleotide phosphodiesterases
CC (PDEs) catalyze the hydrolysis of 3', 5' cyclic nucleotides, such as cAMP
CC and cGMP, to their corresponding 5'-nucleotide monophosphates. The PDEs
CC are therefore important in the control of the cellular concentration of
CC cyclic nucleotides. The PDEs are, in turn, regulated by transmembrane
CC signals or second messenger ligands such as calcium ion or cGMP. The
CC PDEs therefore have a central role in regulating the flow of information
CC from extracellular hormones, neurotransmitters, or other signals that use
CC the cyclic nucleotides as messengers. PDEs are present in most of the
CC cells and tissues of eukaryotic organisms, but only in trace amounts.
CC Cam-PDEs are responsive to intracellular calcium, which leads to a
CC decreased intracellular concentration of cAMP, and/or cGMP. This
CC sequence can be used for the production of recombinant Cam-PDE, which may
CC have therapeutic and diagnostic uses. The encoded protein may also be
CC useful for diagnostic antibody production.
CC (Updated on 25-MAR-2003 to correct PF field.)
XX

SQ Sequence 1844 BP; 417 A; 551 C; 514 G; 362 T; 0 other;

Query Match 43.6%; Score 1347.6; DB 18; Length 1844;
Best Local Similarity 90.6%; Pred. No. 0;
Matches 1473; Conservative 0; Mismatches 144; Indels 9; Gaps 3;

QY 175 GCTGGCTACATGGTGAAGCAGTTCGAGAATGGGAGATAAACATTGAGGAGCTCAAGAA 234
Db 224 GCTGGCTACATGGTGAAGCAGTTCGAGAATGGGAGGATTAACATTGAGGAGCTCAAGAA 283
QY 235 AAATCTGGAGTACACAGCTTCTCTCTGGAAGCCGCTTACATAGATGAGACACGGCAAT 294
Db 284 AAACCTGGAGTACACAGCTTCTCTCTGGAAGCCGCTTATATAGATGAGACTCGCAAT 343
QY 295 CTTGACACGAGGAGGAGCTGCGAGAGCTGCGGTTCAGATGCCGTGCTCGGAGGTGG 354
Db 344 CTTGACACGAGGAGGAGTGCAGAGAGCTGCGGTTCAGATGCCGTGCTCGGAGGTGG 403
QY 355 GGACTGGCTGGCTCCACCTTCCACCCAGCAGCCGCGGCAAGCCGCCAGCAGAGAGA 414
Db 404 GGACTGGCTGGCTCCACCTTCCACCCAGCAGCCGCGGCAAGCCGCCAG---CGAAGA 460
QY 415 GAAGCCCAAGTTCGAAGCATTGTGCACGCTGTGCAGGCTGGGATTCCTTCGTGGAGAG 474
Db 461 GAAGCCCAAGTTCGAAGCATTGTGCACGCTGTGCAGGCTGGGATTCCTTCGTGGAGAG 520
QY 475 GTTCGGAGACATACACCTCTGTGGGCCCCACCTTACTCTACTGCGGTTCCTCAACTGTCT 534
Db 521 GTTCGGAGACATACACCTCTGTGGGCCCCACCTTACTCTACTGCGGTTCCTCAACTGTCT 580
QY 535 CAAGAACCTGGATCTCTGTGGTGTGATGCTTTTCTTGAACACGAGCAGAGATGACCA 594
Db 581 CAAGAACCTGGATCTCTGTGGTGTGATGCTTTTCTTGAACACGAGCAGAGATGACCA 640
QY 595 TGCCCTGAGGACCAATGTTTGTGACTGCTGACTCGGCATACCTTCATCAGCCGCTTCAA 654
Db 641 CGCCCTGAGGACCAATGTTTGTGACTGCTGACTCGGCATACCTTCATCAGCCGCTTCAA 700
QY 655 GATTCCTGAGTGTGTTTGTGAGTGTGCTGATGCTTGGAGAGAGGCTATGGGAAGTA 714
Db 701 GATTCCTGAGTGTGTTTGTGAGTGTGCTGATGCTTGGAGAGAGGCTATGGGAAGTA 760
QY 715 CAAGAATCTTACCAACACAGATCCAGCAGCCGATGTTACCCAGACAGTCTCATTTGCTT 774
Db 761 CAAGAATCTTACCAACACAGATCCAGCAGCCGATGTTACCCAGACAGTCTCATTTGCTT 820
QY 775 CTTGCTCGCACAGGAGTGGTGCATGCTGCTGCGAGATGAGCTTCCTGGCCATCATCTT 834
Db 821 CTTGCTCGCACAGGAGTGGTGCATGCTGCTGCGAGATGAGCTTCCTGGCCATCATCTT 880
QY 835 TGCTGCAGCTATCCATGATGATGAGCAGACAGGGGACTACCAACAGCTTCCACATCCAC 894
Db 881 TGCTGCAGCTATCCATGATGATGAGCAGACAGGGGACTACCAACAGCTTCCACATCCAC 940


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QY 475 GTTCGGAGAACATACACCTCTGTGGGCCCCACCTTACTCTACTGCGGTCTCAACTGTCT 534
DB 521 GTTCGGAGAACATACACCTCTGTGGGCCCCACCTTACTCTACTGCGGTCTCAACTGTCT 580
QY 535 CAAGAACCTGGATCTCTGTGCTGTGTGATGCTTTTCTTTGAGAGAGAGAGAGAGAGAGAG 594
DB 581 CAAGAACCTGGAGCTTTGCTGTGTGATGCTTTTCTTTGAGAGAGAGAGAGAGAGAGAG 640
QY 595 TGCCCTGAGGACCATTTGTTTGTAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 654
DB 641 CGCCCTGAGGACCATTTGTTTGTAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 700
QY 655 GATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 714
DB 701 GATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 760
QY 715 CAAGAACTCTTACCAACACAGATCCAGGACGAGCGATGTTACCCAGAGCTTCATTTGCTT 774
DB 761 CAAGAACTCTTACCAACACAGATCCAGGACGAGCGATGTTACCCAGAGCTTCATTTGCTT 820
QY 775 CTTCCTCGGACAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 834
DB 821 CTTCCTCGGACAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 880
QY 835 TGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 894
DB 881 TGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 940
QY 895 CAAGTCAGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 954
DB 941 CAAGTCAGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1000
QY 955 CTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1014
DB 1001 CTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1060
QY 1015 TGAGTTTGTAGAACTCCGAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1074
DB 1061 TGAGTTTGTAGAACTCCGAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1120
QY 1075 CCATTTCCAGAACTGAGAGACCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1134
DB 1121 CCATTTCCAGAACTGAGAGACCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1180
QY 1135 GCCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1194
DB 1181 GTCCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1240
QY 1195 GTTGGTCCAGAGCCTGTTGAGCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1254
DB 1241 GTTGGTCCAGAGCCTGTTGAGCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1300
QY 1255 GGAGGAGAGTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1314
DB 1301 GGAGGCTGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1360
QY 1315 ACAGTCTCAGATAGGTTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1374
DB 1361 ACAGTCTCAGATAGGTTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1420
QY 1375 CGTGGCAGAGAGAGTGTTCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1434
DB 1421 TGTGGCTGAGAGAGTGTTCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1480
QY 1435 CAGCTTTTCAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1494
DB 1481 CAGCTTTTCAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1540
QY 1495 GGTGAGCTTTGCTTCCAGCTGGGTCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1554
DB 1541 GGTGAGCTTTGCTTCCAGCTGGGTCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1600
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1555 ACGGCGAGCAAGTGGCATCACCACAGATGTCCATTGACGAGTGTCCCTCTGTGAAGA 1614
1601 ACGGCGCGAGCGGCATCACCACAGATGTCCATTGACGAGTGTCCCTCTGTGAAGA 1660
1615 AGAGGCCCGCCATCCCTGCGGAGATGACACACAGAAATGGGAATCTGGATTAGCC 1674
1661 AGAGGCCCGCCATCCCTGCGGAGAGAGACACAGAAATCTGGACTAGC- 1719
1675 CTGGGCTGGCCAGGCTTCTATTGAGTCCAAAGTGTGTTGATGTCATCAGCACCATCCAT 1734
1720 --GGGCGCTGCCAGGCTCTCAGTGTGCTGAGTGTTCGATGTCATCAGCACCATCCAT 1777
1735 CAGGACTGGCTCCCGCATCTCTCACAAGGAGCGTG---GTCGTGGAAGAAACAACCCAC 1791
1778 CGGACTGGCTCCCGCATCTCTCGGAGGCGAATGGATGTCAAGGAACAAGAAACCCAC 1837
1792 CTGAAG 1797
1838 CCGAAG 1843

RESULT 8
AAV54753
ID AAV54753 standard; cDNA; 1844 BP.
XX AAV54753;
AC AAV54753;
XX 29-OCT-1998 (first entry)
XX 63 kDa CaM-PDE DNA from clone p12.3a.
XX Ca2+/calmodulin sensitive cyclic nucleotide phosphodiesterase; CaM-PDE;
XX assay; identification; modification; enzymatic activity; modulator; ss.
XX Bos sp.
XX Key Location/Qualifiers
XX 114..1718
XX /*tag= a
XX /product= CaM-PDE
XX US8600987-A.
XX 01-SEP-1998.
XX 31-MAY-1995; 95US-0455525.
XX 20-APR-1992; 92US-0872644.
XX 19-APR-1991; 91US-0688356.
XX 29-AUG-1994; 94US-0297494.
XX 31-MAY-1995; 95US-0455525.
XX (UNIW) UNIV WASHINGTON.
XX Beavo JA, Bentley JK, Charbonneau H, Sonnenburg WK;
XX WPI; 1998-494762/42.
XX P-PSDB; AAV71223.
XX Identification of modulators of Calcium/calmodulin sensitive cyclic
XX nucleotide phosphodiesterase - uses recombinant cells expressing the
XX enzyme and monitoring protein expression in the presence of
XX potential modulators
XX Example 3; Columns 55-58; 69pp; English.
XX The present sequence encodes the 63 kDa Ca2+/calmodulin sensitive cyclic
XX nucleotide phosphodiesterase (CaM-PDE) from bovine brain. CaM-PDE enzymes
XX catalyse the hydrolysis of cyclic nucleotides and as such control their
XX intracellular level. They are controlled by second messengers e.g. Ca2+
XX and calmodulin and transmembrane signals and through pathways involving
XX these, regulate flow of information from extracellular hormones,
XX neurotransmitters and other signals using cyclic nucleotides as

CC messengers. The specification describes an assay for identifying a
CC chemical agent which modifies the enzymatic activity of a mammalian
CC Cam-PDE. The assays are useful for identifying modulators of Cam-PDEs.
CC The assay is carried out by incubating cells expressing Cam-PDE with the
CC suspected modulator and measuring its effect e.g. monitoring the
CC hydrolysis of cAMP and/or cGMP.
XX
SQ Sequence 1844 BP; 417 A; 551 C; 514 G; 362 T; 0 other;

Query Match 43.6%; Score 1347.6; DB 19; Length 1844;
Best Local Similarity 90.6%; Pred. No. 0;
Matches 1473; Conservative 0; Mismatches 144; Indels 9; Gaps 3;

Qy 175 GTCGCTACATGGTGAAGCAGTTCCTGCTGGAAGCCGCTACATAGATGAGAGTGAAGAA 234
Db 224 GCTGCGCTACATGGTGAAGCAGTTCCTGCTGGAAGCCGCTACATAGATGAGAGTGAAGAA 283
Qy 235 AAATCTGGAGTACACAGCTTCCTGCTGGAAGCCGCTACATAGATGAGAGTGAAGAA 294
Db 284 AAACCTGGAGTACACAGCTTCCTGCTGGAAGCCGCTACATAGATGAGAGTGAAGAA 343
Qy 295 CTGGACAGGAGGAGTGCAGAGCTGCGGTCAGATGCGCTTCGGAGGTGCG 354
Db 344 CTGGACAGGAGGAGTGCAGAGCTGCGGTCAGATGCGCTTCGGAGGTGCG 403
Qy 355 GGAAGTGGCTGCTCCACCTTCACCCAGCAGCCGCGGCAAGGCGCCGAG 414
Db 404 GGAAGTGGCTGCTCCACCTTCACCCAGCAGCCGCGGCAAGGCGCCGAG 460
Qy 415 GAAGCCCAAGTTCGCAAGCATTCGACGCTGTCAGGCTGGGATCTTCGGAACGAT 474
Db 461 GAAGCCCAAGTTCGCAAGCATTCGACGCTGTCAGGCTGGGATCTTCGGAACGAT 520
Qy 475 GTTCGGGAAATACACCTCTGTGGGCGCCACTTACTTCTACTGGGTTCTCACTGTC 534
Db 521 GTTCGGGAAATACACCTCTGTGGGCGCCACTTACTTCTACTGGGTTCTCACTGTC 580
Qy 535 CAAGAAGCTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 594
Db 581 CAAGAAGCTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 640
Qy 595 TGCCCTGAGGACCATTTGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 654
Db 641 CGCCCTGAGGACCATTTGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 700
Qy 655 GATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 714
Db 701 GATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 760
Qy 715 CAAGAATCTTACCAACCAAGATCCAGCGCCGATGTTACCCAGACAGTCCCATGCTT 774
Db 761 CAAGAATCTTACCAACCAAGATCCAGCGCCGATGTTACCCAGACAGTCCCATGCTT 820
Qy 775 CTGCTCCGACAGGAGTGGTGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 834
Db 821 CTGCTCCGACAGGAGTGGTGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 880
Qy 835 TGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 894
Db 881 TGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 940
Qy 895 CAAGTTCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 954
Db 941 CAAGTTCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1000
Qy 955 CTCTGCTTTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1014
Db 1001 CTCTGCTTTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1060
Qy 1015 TGAGTTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1074
Db 1061 TGAGTTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1120

Qy 1075 CCATTTCCAGCAGTGAAGACCATGAAGACAGAGCCCTTCCAAACAGCTGGAGGATTGACAA 1134
Db 1121 CCATTTCCAGCAGTGAAGTCCATGAAGACAGAGCCCTTCCAAACAGCTGGAGGATTGACAA 1180
Qy 1135 CCAAGGCGCTGCTCTACTGCTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1194
Db 1181 CCAAGGCGCTGCTCTACTGCTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1240
Qy 1195 CCAAGGCGCTGCTCTACTGCTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1254
Db 1241 CCAAGGCGCTGCTCTACTGCTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1300
Qy 1255 GAGGCGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1314
Db 1301 GAGGCGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1360
Qy 1315 ACAGTTCAGATGAGGTTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1374
Db 1361 ACAGTTCAGATGAGGTTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1420
Qy 1375 CAGGCGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1434
Db 1421 CAGGCGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1480
Qy 1435 CAGGCGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1494
Db 1481 CAGGCGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1540
Qy 1495 GGTGCGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1554
Db 1541 GGTGCGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1600
Qy 1555 ACAGGCGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1614
Db 1601 ACAGGCGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1660
Qy 1615 AGAGGCGCGCCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1674
Db 1661 AGAGGCGCGCCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1719
Qy 1675 CTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1734
Db 1720 CTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1777
Qy 1735 CAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1791
Db 1778 CAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1837
Qy 1792 CTGAAG 1797
Db 1838 CCGAAG 1843

RESULT 9

AAV36148
ID AAV36148 standard; cDNA; 1844 BP.

XX AAV36148;

XX 07-SEP-1998 (first entry)

XX Bovine Cam-PDE encoding a 63 kDa protein.
XX

XX Bovine: decrease; intracellular concentration; cAMP; cGMP;
XX calcium/calmodulin stimulated cyclic nucleotide phosphodiesterase;
XX Cam-PDE; therapy; prognosis; diagnosis; specific modulator;
XX Cam-PDE activity; identification; signalling; extracellular hormone;
XX neurotransmitter; selective inhibitor; cardioconic; antidepressant;
XX antihypertensive; antithrombotic agent; ss.

XX Bos sp.

XX Key Location/Qualifiers
FH

[illegible]

Db 1181 GTCAAGCCCTCTCTCTGCTTCACTGCTGACATCAGCACCCACCAAGCAGTG 1240
QY 1195 GTTGTGCACAGCGTGGAGCAAGGCCCTCATGGAGGAATCTTCCCTCAGGCTGACAA 1254
Db 1241 GTGCGTTCACAGCGCTGGAGCAAGGCCCTCATGGAGGAATCTTCCGCCAGGCTGACAA 1300
QY 1255 GGAGCGAGAGTTGGCGCTGCCCTTTCTTCCACTCTGTGACCGCACTTCCACTCTAGTGGC 1314
Db 1301 GGAGCGTGTGCGCTGCCCTTTCTTCCACTCTGTGACCGCACTTCCACTCTAGTGGC 1360
QY 1315 ACAGTCTCAGATAGGTTTCATCGACTTATGTGGAGCCCACTTCTCTGTGCTGACATG 1374
Db 1361 GCAGTCCAGATAGGTTTCATCGACTTATGTGGAGCCCACTTCTCTGTGCTGACATG 1420
QY 1375 CGTGCAGAGAGAGTGTTCAGCCCTTGGCGGATCAGGACTTCAAGTCTAATAACCCAGCC 1434
Db 1421 TGTGCTGAGAGAGTGTTCAGCCCTTGGCGGATCAGGACTTCAAGTCTAATAACCCAGCC 1480
QY 1435 CAGCTTTTTCAGTGGCGCCAGCCCTCTCTGATGTGGAAGTGGAGACCCCAACCCCTGATGT 1494
Db 1481 CAGCTTCCAGTGGCGCCAGCCCTCTCTGATGTGGAAGTGGAGACCCCAACCCCTGATGT 1540
QY 1495 GGTGAGCTTCTGCTCCAGCTGGTCAAGCCGATTCAGGAGAAATAGCAGAAATGAAGGA 1554
Db 1541 GGTGAGCTTCTGCTCCAGCTGGTCAAGCCGATTCAGGAGAAATAGCAGAAATGAAGGA 1600
QY 1555 ACGGCGACGAAGTGTTCAGCCCTTGGCGGATCAGGACTTCAAGTCTAATAACCCAGCC 1614
Db 1601 ACGGCGGAGAGGCTTCAAGCCCTTGGCGGATCAGGACTTCAAGTCTAATAACCCAGCC 1660
QY 1615 AGAGGCCCTCCCTCCCTGCGGAGTGAACCAACCAAGTGGAGTTCGATTCGATTCGATTC 1674
Db 1661 AGAGGCCCTCCCTCCCTGCGGAGTGAACCAACCAAGTGGAGTTCGATTCGATTCGATTC 1719
QY 1675 CTGGGCTGGCCAGGCTTTCATGAGTCCAAAGTGTTCATGATTCATGATTCATGATTCAT 1734
Db 1720 --GGGCGCTGGCCAGGCTTTCATGAGTCCAAAGTGTTCATGATTCATGATTCATGATTCAT 1777
QY 1735 CAGGACTGGCTCCCTCCCTGCTCAGAGGAGCGTG---GTCGTGGAAGAAACCAACCCAC 1791
Db 1778 CGGAGTGGCTCCCTCCCTGCTCAGAGGAGCGTG---GTCGTGGAAGAAACCAACCCAC 1837
QY 1792 CTGAAG 1797
Db 1838 CCGAAG 1843

RESULT 11
ABX78849
ID ABX78849 standard; cDNA; 1844 BP.
XX AC ABX78849;
XX
DT 15-APR-2003 (first entry)
DE Bovine brain cDNA encoding 63kDa CaM-PDE variant #1.
DE
XX
KW Cow; ss: Ca2+/calmodulin stimulated phosphodiesterase;
KW CaM-PDE; 59kDa CaM-PDE; 61kDa CaM-PDE; 63kDa CaM-PDE; CGS-PDE;
KW cyclic-GMP-stimulated phosphodiesterase; cardiotonic agent;
KW antipressant; anti-hypertensive; anti-thrombotic.
XX
OS Bos taurus.
XX
PN US2002151024-A1.
XX
PD 17-OCT-2002.
XX
PF 18-JUN-2001; 2001US-0883825.
XX
PR 20-APR-1992; 92US-0872644.
PR 31-MAY-1995; 95US-0455526.
PR 28-JUL-1998; 98US-0123783.

PR 19-APR-1991; 91US-0688356.
XX (UNIW) UNIV WASHINGTON.
PI Beavo JA, Bentley JK, Charbonneau H, Sonnenburg WK;
XX WPI; 2003-198291/19.
DR P-PSDB; ABU58716.
XX
PT New purified and isolated DNA sequence encoding a mammalian
PT calcium/calmodulin- or cyclic GMP-stimulated cyclic nucleotide
PT phosphodiesterase polypeptide, useful for therapeutic, diagnostic and
PT prognostic applications
XX
PS Example 3; Page 30-32; 71pp; English.
XX
CC The invention relates to purified and isolated polynucleotide sequence
CC encoding a mammalian Ca²⁺/calmodulin- or cyclic GMP-stimulated cyclic
CC nucleotide phosphodiesterase polypeptide (CaM-PDE and CGS-PDE).
CC Also included are a DNA vector comprising the novel DNA sequence, a host
CC cell transformed with the polynucleotide sequence, a polypeptide product
CC of the expression in the transformed host cell, an antibody specifically
CC immunoreactive with the polypeptide and assay methods for identifying a
CC chemical agent which modifies the enzymatic activity of a mammalian
CC CaM-PDE or CGS-PDE. Disclosed are the cDNA and protein sequences
CC of bovine 59kDa CaM-PDE, 61kDa CaM-PDE, 63kDa CaM-PDE, CGS-PDE and
CC human 61kDa CaM-PDE and CGS-PDE. The DNA sequence is useful for producing
CC a polypeptide having the enzymatic activity of a mammalian CaM-PDE or
CC CGS-PDE which is used in therapeutic, diagnostic and prognostic
CC applications and in the preparation of antibodies. Isolated chemical
CC agents which are inhibitors of PDEs may have anti-depressant, anti-
CC hypertensive or anti-thrombotic activities or may be cardiotonic agents.
CC The present sequence is a Bovine cDNA (or fragment) encoding a
CC CaM-PDE or CGS-PDE of the invention.
XX
SQ Sequence 1844 BP; 417 A; 551 C; 514 G; 362 T; 0 other;
Query Match 43.6%; Score 1347.6; DB 25; Length 1844;
Best Local Similarity 90.6%; Pred. No. 0;
Matches 1473; Conservative 0; Mismatches 144; Indels 9; Gaps 3;
QY 175 GCTGCGCTACATGTGGAAGCAGTGTGGAGAAATGGGAGATTAACATTTGAGAGCTGAAGAA 234
Db 224 GCTGCGCTACATGTGGAAGCAGTGTGGAGAAATGGGAGGTTAAACATTTGAGAGCTGAAGAA 283
QY 235 AAATCTGAGTACACAGCTTCTCTGGAAGCCCTCTACATAGATGAGACACGCAAT 294
Db 284 AAACCTGGAGTACACAGCTTCTCTGGAAGCCCTCTATATAGATGAGACTCGGCAAT 343
QY 295 CTTGGACACGGAGACAGCTGCGGTCAGATGCGCTTCGAGGTGCG 354
Db 344 CTTGGACACGGAGATGAGCTGCGGTCGATGCGGTGCTGATGCGGTGCTGAGAGTGGC 403
QY 355 GGAATGCTGCGCTCCACCTTACCCAGACGCGCGGCGCAAGCCCGGAGCAGAGGA 414
Db 404 GGAATGCTGCGCTCCACCTTACCCAGACGCGCGGCGCAAGCCCGGAG---CGAAGA 460
QY 415 GAAGCCCAAGTTCGGAAGCATGTGACGCTGTGAGGCTGGATTCGTTGGAACGGAT 474
Db 461 GAAGCCCAAGTTCGGAAGCATGTGACGCTGTGAGGCTGGATTCGTTGGAACGGAT 520
QY 475 GTTCCGGAGAAATACATACCTCTGTGGGCGCCCACTTACTCTACTGCGGTCTCAACTGTCT 534
Db 521 GTTCCGGAGAAATACATACCTCTGTGGGCGCCCACTTACTCTACTGCGGTCTCAACTGTCT 580
QY 535 CAAGAACCTGGATCTCTGGTGTGTGTGTCTTTTCTTGAACACGAGGACGAGATGACCA 594
Db 581 CAAGAACCTGGATCTCTGGTGTGTGTGTCTTTTCTTGAACACGAGGACGAGATGACCA 640
QY 595 TGCCCTGAGGACCATTTTGTGAGTGTGCTGACTCGGCATACCTTCATCAGCCGCTTCAA 654
Db 641 CGCCCTGAGGACCATTTTGTGAGTGTGCTGACTCGGCATACCTTCATCAGCCGCTTCAA 700

Db	344	CCTGGACGAGAGTGAAGTCTGAGAGTCTGCGGTCTGATCGGTGCGTTCAGAGGTGCG	403
QY	355	GGACTGGCTGGCTCCACCTTCACCCAGCAGCCGCGGCCCAAGGCGCCGAGCAGAGGA	414
Db	404	GGACTGGCTGGCTCCACCTTCACCCAGCAGCCGCGGCCCAAGGCGCCGAG	460
QY	415	GAAGCCCAAGTTCCGAAGCATTTGTCAGCGCTGTGCGAGCTGGGATCTTCGTGGAAACGAT	474
Db	461	GAAGCCCAAGTTCCGAAGCATTTGTCAGCGCTGTGCGAGCTGGGATCTTCGTGGAAACGAT	520
QY	475	GTTCGGGAGAAATACACTCTGTGGGCGCCCACTTACTCTACTCTGCGGTTCCTCAACTGTCT	534
Db	521	GTTCGGGAGAAATACACTCTGTGGGCGCCCACTTACTCTACTCTGCGGTTCCTCAACTGTCT	580
QY	535	CAAGAACCTGGATCTCTGGTGGTCTGATGCTCTTTTCCCTTGAACAGCAGCAGATGACCA	594
Db	581	CAAGAACCTGGATCTCTGGTGGTCTGATGCTCTTTTCCCTTGAACAGCAGCAGATGACCA	640
QY	595	TGCGCTGAGGACCATTTTGTAGTCTGTGACTCGGCATTAACCTCATCAAGCCGCTTCAA	654
Db	641	CGCCCTGAGGACCATTTTGTAGTCTGTGACTCGGCATTAACCTCATCAAGCCGCTTCAA	700
QY	655	GATTCACCATGTCTTTTGTAGTCTGTGACTCGGCATTAACCTCATCAAGCCGCTTCAA	714
Db	701	GATTCACCATGTCTTTTGTAGTCTGTGACTCGGCATTAACCTCATCAAGCCGCTTCAA	760
QY	715	CAAGAACCTTTACCAACACCATCCAGCAGCCGATGTTACCCAGCAGTCCATTTGCTT	774
Db	761	CAAGAACCTTTACCAACACCATCCAGCAGCCGATGTTACCCAGCAGTCCATTTGCTT	820
QY	775	CTTGCTCCGACAGGAGTGTGCACTGCTGTGCGAGATTGAGCTCTCGGCCATCATCTT	834
Db	821	CTTGCTCCGACAGGAGTGTGCACTGCTGTGCGAGATTGAGCTCTCGGCCATCATCTT	880
QY	835	TGCTGAGCATATCCATGATATGAGCAGCAGCGGCATCAACAGCTTCCACATCCAGAC	894
Db	881	TGCTGAGCATATCCATGATATGAGCAGCAGCGGCATCAACAGCTTCCACATCCAGAC	940
QY	895	CAAGTCAGAAATGTCATGCTGTGCAATGATGCTGCTGAGAGATCAACACATCAG	954
Db	941	CAATCGGAATGCGGCATCTGTACAGCAGCGCTGAGTGTGAGAGATCAACACATCAG	1000
QY	955	CTCTGTTTCCGATTTGATCAGGATGATGAGATGAACATTTTTCATCAACCTCAACCAAGGA	1014
Db	1001	CTCGGTTTTCCGAATGATGTCAGGACGAGAGATGAACATTTTTCATCAACCTCAACCAAGGA	1060
QY	1015	TGAGTTTGTAGAACTCCGAGCCCTGGTCTGATGAGATGTTGTCAGCAGACATGTCCTG	1074
Db	1061	TGACTTTGTAGAACTCCGAGCCCTGGTCTGATGAGATGTTGTCAGCAGACATGTCCTG	1120
QY	1075	CCATTTCCAGCAAGTGAAGACCATCAAGCAGCCCTTGCAACAGCTGGAGAGATTGACAA	1134
Db	1121	CCATTTCCAGCAAGTGAAGTCCATGAAGCAGCCCTTGCAACAGCTGGAGAGATTGACAA	1180
QY	1135	GCCCAAGGCCCTGTCTACTGCTCCATGCTGCTGACATCAGCCACCCCAACCAAGCAGTG	1194
Db	1181	GTCCAAGGCCCTGTCTACTGCTCCATGCTGCTGACATCAGCCACCCCAACCAAGCAGTG	1240
QY	1195	GTTGGTCCACAGCGTTGACCAAGCCCTCATGAGGAAATTTTCGCTCAGGTTGACAA	1254
Db	1241	GTCGGTTCCACAGCGTTGACCAAGCCCTCATGAGGAAATTTTCGCTCAGGTTGACAA	1300
QY	1255	GGAGGAGAGTTGGCGCTGCTTCTTCCACTCTGTGACCGCAGCTTCCACTCTAGTGGC	1314
Db	1301	GGAGGCTGAGCTGGCGCTGCTTCTTCCGCTCTGTGACCGCAGCTTCCACTCTAGTGGC	1360
QY	1315	ACAGTCTCAGATAGGTTTCATCGACTTCATTTGTGGAGCCCACTTCTGTGCTGACTGA	1374
Db	1361	GCAGTCCAGATGTTTTCATCGACTTCATTTGTGGAGCCCACTTCTGTGCTGACTGA	1420
QY	1375	CGTGCGAGAGAGTGTTCAGCCCTTGGCGGATGAGGACTCCCAAGTCTAAAAACACGAC	1434

Claim 2; Columns 109-114; 69pp; English.

AAQ83981 encodes AAR69732 the human cyclic-GMP stimulated nucleotide phosphodiesterase (Cam PDE) clone pcam3HEF. Eukaryotic cells that express Cam PDE can be used to screen cpds. for the ability to modulate Cam PDE activity. Cam PDEs are involved in regulating the transmission of information from hormones, neurotransmitters or other systems that use cyclic nucleotides as messengers. Antibodies raised against Cam PDE can be used for enzyme purification or determination. (Updated on 25-MAR-2003 to correct PF field.)

Sequence 2693 BP; 777 A; 618 C; 651 G; 647 T; 0 other;

Query Match 19.3%; Score 598; DB 16; Length 2693;

Best Local Similarity 67.9%; Pred. NO. 2.6e-150;
Matches 851; Conservative 0; Mismatches 400; Indels 3; Gaps 1;

173	QY	AGGCTGCCCTACATGGTGAAGCAGTTGGAGATGGGGAGATAAACATTGAGAGCCTGAAG	233
302	Db	AGATTACGGTCTTTGGTCAACAACAAATAGAGAGAGGGAAAGCTTCAGTGGTAGATCTTTAAG	361
233	QY	AAAAATCTGGAGTACACAGCTTCTCTGCTGGAAGCCGCTACATAGATGAGACACAGCGAA	292
362	Db	AAGAAATTTGGAAATATGACGCCACAGCTGCTTGAATCTGTGTATATTGATCAACAAGGAGA	421
293	QY	ATCTTGGACACGGAGGACGAGCTGCAAGAGCTCGGCTCAGATGCCGTGCTTCCGAGGTG	352
422	Db	CTCCTGGATACAGAGGATGAGCTCAGTGCATTCAGTCAGATGCTGCTCTCTGAGTCT	481
353	QY	CGGACTGGCTGGCCCTCCACCTTCACCCACGACAGCCCGGCCCAAGGCCGCGGACGAG	412
482	Db	CGAGACTGGCTGGCCCTCCACCTTCACCGGCAGATGGGATGATGCTCAGGAGNGCGAC	541
413	QY	GAGAGGCCAAGTTCCGAAGCANTGTGCACGCTGTGCAGGCTGGGATCTTCGTGGAACGG	472
542	Db	GGAAGCCCCGGTTCAAGCAATCGTTACGACGAGTGCAGGCTGGGATATTGTGGAGAGA	601
473	QY	ATGTTCCGGAGAACATACACACTCTGTGGGCCCCACTTACTCTACTGCGGTTCTCAACTGT	532
602	Db	ATGTATAGCGGACATCAAAACATGGTTGGACTGAGCTATCCACCAGCTGTTATTGAGGCA	661
533	QY	CTCAAGAACCTGGGATCTCTGGTGCTTTGATGTCTTTTCTTGAACCAGGCGACGACATGAC	592
662	Db	TTAAAGGATGTGGAAACAGTGGTCTTTTGACGTCTTTTCCGCTCAATGAGCGCAGTGGGAT	721
593	QY	CATGCCCTGAGGACCATTTGTTTGTGAGTTGCTGACTCGGCATAAACCTCATCAGCGGTTTC	652
722	Db	CATGCACTGAAATTAATTTTCTATGAACACTCACACGTTATGATCTGATCAGCGGTTTC	781
653	QY	AAGATTCCCACTGTTTTGTGATGAGTTTCTCTGGATGCTTGGACACAGGCTATTTGGGAAG	712
782	Db	AAGATCCCACTTTCTGCACCTTCTCATTTGTGGAGGCCCTGGAAGTGGATACGCAAG	841
713	QY	TACAAAGATCCTTACCACACACAGATCCACGACGCGGATGTACCACACAGTCCATGTC	772
842	Db	CACAAATCCTTACCATAACTTAATGCACGCTGCCGATGTTACACACAGTGCATTC	901
773	QY	TTCTTGTCGCCACAGGATGTGCACTGCCTGTGCGAGATTTAGCTCTCTGCCCATCATC	832
902	Db	CTCCTCTTAAGACGAGGTGGGAACTGGCTGACGGAGCTGGAGATCTTTGCTATATTC	961
833	QY	TTTGCTGCAGCTATCCAAATGATATGACACACAGGGCACTTACCAACAGCTTCCACATCCAG	892
962	Db	TTCTCAGCTGCCATCCCAATGACTACGAGCATACCGAAACCAACAATTTCCACATTCAG	1021
893	QY	ACCAAGTCAGAAATGTGCCATCGTGTACAATGATCGTTCAGTGTGGAGAATCACCAATC	952
1022	Db	ACTCGGCTGATCCAGCTATCTTGTTAATATGACAGATCTGACTGGAGAACTCACCATTTA	1081
953	QY	AGCTCTGTTTTCCGATTGATGACAGGATGATGAG---ATGAACATTTTCATCAACCTCAC	1009
1082	Db	AGTCAGCTTATCGCCTTCTGCAAGATGACGAGGAAATGAATATTTGATTAACCTCTCA	1141

CC The present sequence encodes a 61 kDa Ca^{2+} /calmodulin-stimulated
CC cyclic nucleotide phosphodiesterase (CAM-PDE) enzyme derived from
CC human brain. The DNA sequences are used for the production of the
CC recombinant enzymes, which in turn may be used for antibody
CC production and to screen for compounds that modulate phosphodiesterase
CC activity.
CC (Updated on 25-MAR-2003 to correct PF field.)
CC (Updated on 25-MAR-2003 to correct PI field.)
xx
SQ Sequence 2693 BP; 777 A; 618 C; 651 G; 647 T; 0 other;

Query Match	19.3%	Score 598	DB 18	Length 2693
Best Local Similarity	67.9%	Pred. No. 2.6e-150		
Matches 851	Conservative 0	Mismatches 400	Indels 3	Gaps 1
QY	173	AGGCTGGCTACATGTTGAAGCAGTGGGAAATGGGGAGATAAACATTTGAGGAGCTGAAG	232	
DB	302	AGATTACGGTCTTTGGTCAACAAATATAGAGAGAGGGAAGCTTCAGTGGTAGATCTTAAG	361	
QY	233	AAAAATCTGGAGTACACAGCTTCTCTCTGGAAAGCCGCTTACATAGATGAGACAGGCAA	292	
DB	362	AAGAAATTTGGAATATGCAGCCACAGTGCCTTGAATCTGTGTATATGATGAACAAGGAGA	421	
QY	293	ATCTTGACACAGGAGACAGCTGACAGGAGCTGCGGTACAGATCCGCTGCTCGGAGGTG	352	
DB	422	CTCCTGATACAGAGATGATGCTCAGTGACATTCAGTCAGATGTGTGCTTCTTGAGGTC	481	
QY	353	CGGAGCTGGCTGGCTCCACCTTCACCCACGAGCGCCGGGCCAAAGCCGCCGACAGAG	412	
DB	482	CGAGACTGGCTGGCTCCACCTTCACCGGCACATGGGGATGATGCTCAGGAGGAGCGCAC	541	
QY	413	GAGAAGCCCAAGTTCCGAAGCATGTGCACGCTGTGCAGGCTGGGATCTTCGTGGAAACGG	472	
DB	542	GAGNAGCCCGGTTCAAGACATCGTTACAGCAGTGCAGGCTGGGATATTTGTGGAGAGA	601	
QY	473	ATGTTCCGGAGAACATACACCTCTGTGGGGCCCACTTACTCTACTCGGCTTCACAACTGT	532	
DB	602	ATGTATAGCGGACATCAAAACATGGTTGGACTGAGCTATCCACAGCTGTTATTGAGGCA	661	
QY	533	CTCAGAAACCTGATCTCTGGTGTGTGATGCTCTTTCTTGTGAACGAGCAGATGAC	592	
DB	662	TTAAGGATGTGACAAAGTGGTCTCTTTGAGCGTCTTTCCCTCAATGAGGCCAGTGGGAT	721	
QY	593	CATGCGCTGAGGACCATTTGTTTGTAGCTGCTGACTCGGCATACCTCATCAGCCGCTTC	652	
DB	722	CATGCACTGAAATTTATTTTCTATGAACACTACTCACAGCTTATGATCGATCAGCCGGTTC	781	
QY	653	AAGATTTCCCACTGTGTTTGTATGAGTGTTCCTCGATGCCTTGGAGACAGGCTATGGGAAG	712	
DB	782	AAGATCCCCATTTCTGCACTTGCTCATTTGTGGAGGCCCTGGNAGTGGGATACAGCAAG	841	
QY	713	TACAAGAAATCCTTACCAACACAGATCCACGCGACCGATGTTACCCACAGATGCCATTCG	772	
DB	842	CACAAAAATCCTTACCATAACTTAAATGACGCTGCCGATGTTACACAGACAGTGCATTAC	901	
QY	773	TTCTTGCTCCGACAGGATGTTGCTCACTGCTGCGGAGATTGAGCTCTCGGCCATCATC	832	
DB	902	CTCCTCTATAAGACAGGAGTGGGGAATGGCTGACGAGCTGGAGATCTTTGCTATAAATC	961	
QY	833	TTTGCTGCAGCTATCCATGATATGACACACAGGGCACTACCAACAGCTTCCACATCCAG	892	
DB	962	TTTCAGCTGCCATCCATGACTAGAGCATACCGGAACCCACAAATTTCCACATTCAG	1021	
QY	893	ACCAAGTCAGAATGTGCCATCTGTGTACAATGATGCTTGTGCTGAGAGATACCACATCC	952	
DB	1022	ACTCGGCTGATCCAGCTATCTGTATPAATGACAGATCTGTACTGGAGAATCACCAATTA	1081	
QY	953	AGCTCTGTTTTCCGATTGATGACGAGTATGAG---ATGAACATTTTCATCAACCTCAC	1009	
DB	1082	AGTGCACCTTATCGCTTCTGCAAGATGACGAGGAATGAATATTTGATTACCTCTCA	1141	
QY	1010	AAGATGAGTTGTGAGAACTCCGAGCCCTGGTCAATTGAGATGTGTTGGCCACAGACAT	1069	

Db	1142	AAGGATGACTGGAGGGAGTTTCGAAACCCTTGGTAAATTGAAATGGTGATGGCCACAGATATG	1201		
Qy	1070	TCCTGCCATTTCCAGCAAGTGAAGACCATGAAGACAGCCTTGGCAACAGCTGGAGAGGATT	1129		
Db	1202	TCITGTCTACTTCCAACAATCAAGCAATGAGACTGCTCTGCAGCAGCCAGAGCCATT	1261		
Qy	1130	GACAAGCCCCAAGGCCCTGTCTTACTGCTCCATGCTGCTGACATCATACGCCACCCACCAAG	1189		
Db	1262	GAAGAAGCAAAAGCCTTATCCCTTATGCTGTGATACAGCAGATATTAGCCATCCAGCAAAA	1321		
Qy	1190	CAGTGGTTGGTCCACAGCCGTTGGACCAAGCCCTCATGGAGGAATTTCTCCGTCAGGGT	1249		
Db	1322	GCATGGGACCTTCCATCATCGCTGACCAATGTCATCTCTGGAGGAGTTCTTTCAGACAGGT	1381		
Qy	1250	GACAAGGAGGAGAGTTGGGCGCTGCCCTTTTCTCCACTCTGTGACCGCACTTCCACTCTA	1309		
Db	1382	GACAGAGAAGCAGAGCTGGGCGTGGCTTTTCTCTCTGTGTGACCGAAAGTCCACTATG	1441		
Qy	1310	GTGGCAGAGTCTCAGATAGGTTTCATCGACTTCAATGTGGAGCCCACTTCTCTGTGCTG	1369		
Db	1442	GTTGCTCAGTCACAAAGTAGTTTCATTTGATTTTCATGTCGTGGAACCCACTTCACTGTGCTT	1501		
Qy	1370	ACTCAGCTGGCAGAGAAGTGTTCAGCCCTCGCGATGAGGACTCCAAAGTCT	1423		
Db	1502	ACGGACATACCGAAGAGTTGTGAGTCCATTAATCGATGAACCTCTCAACT	1555		
RESULT 15					
AAAT51116					
ID	AAAT51116 standard; cDNA; 2693 BP.				
XX	AC	AAAT51116;			
XX	DT	25-MAR-2003 (updated)			
XX	DT	17-MAR-1997 (first entry)			
DE	Hippocampus calcium/calmodulin dependent phosphodiesterase cDNA #2.				
KW	Cyclic GMP stimulated phosphodiesterase; CGS-PDE; bovine; brain; cAMP;				
KW	adrenal gland; transmembrane signal; extracellular hormone; antibody;				
KW	neurotransmitter; cGMP; calcium/calmodulin dependent phosphotriesterase;				
KW	CaM-PDE; human; ss.				
OS	Homo sapiens.				
XX	Key	Location/Qualifiers			
XX	FT	176..2080			
XX	FT	/*tag= a			
XX	FT	/product= calcium/calmodulin dependent phosphodiesterase			
PN	US5580771-A.				
XX	PD	03-DEC-1996.			
XX	PF	29-AUG-1994; 94US-0297494.			
XX	PR	20-APR-1992; 92US-0872644.			
PR	19-APR-1991; 91US-0688356.				
PR	29-AUG-1994; 94US-0297494.				
XX	(UNIW) UNIV WASHINGTON.				
XX	PA	Beavo JA, Charbonneau H, Sonnenburg WK;			
PI	WPI; 1997-033573/03.				
DR	P-PSDB; AAW11256.				
XX	DNA encoding cGMP-stimulated phosphodiesterase - for prodn. of				
PT	recombinant enzyme				
XX	Example 7; Column 109-114; 68pp; English.				
PS	This sequence represents the coding sequence for the calcium/calmodulin				
CC					

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OM nucleic - nucleic search, using sw model

Run on: August 10, 2003, 17:35:00 ; Search time 201 Seconds
(without alignments)
6787.638 Million cell updates/sec

Title: US-09-663-481-2
Perfect score: 3091
Sequence: 1 gtcgaccacgcgtccggga.....aaaaaaaaaaaaaaaaaaaa 3091

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA.*
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
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4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2106.8	68.2	2265	2	US-08-940-332-1
2	1347.6	43.6	1844	1	Sequence 1, Appli
3	1347.6	43.6	1844	1	Sequence 26, Appl
4	1347.6	43.6	1844	1	Sequence 26, Appl
5	1347.6	43.6	1844	1	Sequence 26, Appl
6	1347.6	43.6	1844	1	Sequence 26, Appl
7	1347.6	43.6	1844	1	Sequence 26, Appl
8	1347.6	43.6	1844	3	Sequence 26, Appl
9	1347.6	43.6	1844	5	Sequence 26, Appl
10	598	19.3	2693	1	Sequence 50, Appl
11	598	19.3	2693	1	Sequence 50, Appl
12	598	19.3	2693	1	Sequence 50, Appl
13	598	19.3	2693	1	Sequence 50, Appl
14	598	19.3	2693	1	Sequence 50, Appl
15	598	19.3	2693	1	Sequence 50, Appl
16	598	19.3	2693	3	Sequence 50, Appl
17	598	19.3	2693	5	Sequence 50, Appl
18	579.8	18.8	2656	1	Sequence 16, Appl
19	579.8	18.8	2656	1	Sequence 16, Appl
20	579.8	18.8	2656	1	Sequence 16, Appl
21	579.8	18.8	2656	1	Sequence 16, Appl
22	579.8	18.8	2656	1	Sequence 16, Appl
23	579.8	18.8	2656	1	Sequence 16, Appl
24	579.8	18.8	2656	3	Sequence 16, Appl
25	579.8	18.8	2656	5	Sequence 16, Appl
26	578.8	18.7	1625	1	Sequence 48, Appl
27	578.8	18.7	1625	1	Sequence 48, Appl

28	578.8	18.7	1625	1	US-08-297-510-48	Sequence 48, Appl
29	578.8	18.7	1625	1	US-08-479-532-48	Sequence 48, Appl
30	578.8	18.7	1625	1	US-08-455-526-48	Sequence 48, Appl
31	578.8	18.7	1625	1	US-08-455-525-48	Sequence 48, Appl
32	578.8	18.7	1625	3	US-09-139-431-48	Sequence 48, Appl
33	578.8	18.7	1625	5	PCT-US92-03222-48	Sequence 48, Appl
34	559.6	18.1	2291	1	US-07-872-644-5	Sequence 5, Appl
35	559.6	18.1	2291	1	US-08-297-494-5	Sequence 5, Appl
36	559.6	18.1	2291	1	US-08-297-510-5	Sequence 5, Appl
37	559.6	18.1	2291	1	US-08-479-532-5	Sequence 5, Appl
38	559.6	18.1	2291	1	US-08-455-526-5	Sequence 5, Appl
39	559.6	18.1	2291	1	US-08-455-525-5	Sequence 5, Appl
40	559.6	18.1	2291	3	US-09-139-491-5	Sequence 5, Appl
41	559.6	18.1	2291	5	PCT-US92-03222-5	Sequence 5, Appl
42	449.6	14.5	2077	1	US-07-872-644-52	Sequence 52, Appl
43	449.6	14.5	2077	1	US-08-297-494-52	Sequence 52, Appl
44	449.6	14.5	2077	1	US-08-297-510-52	Sequence 52, Appl
45	449.6	14.5	2077	1	US-08-479-532-52	Sequence 52, Appl

ALIGNMENTS

RESULT 1
US-08-940-332-1
Sequence 1, Application US/08940332
Patent No. 5885834
GENERAL INFORMATION:
APPLICANT: Epstein, Paul M.
TITLE OF INVENTION: SYNTHESIS OF ANTISENSE
TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE OF PHOSPHODIESTERASE AND
TITLE OF INVENTION: INDUCEMENT OF APOPTOSIS IN HUMAN LYMPHOBLASTOID CELLS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESSES:
ADDRESSEE: ALIX, YALE & RISTAS, LLP
CITY: HARTFORD
STATE: CT
COUNTRY: USA
ZIP: 06103-2721
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,332
FILING DATE: 30-SEP-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/027,207
FILING DATE: 30-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Alix, James E.
REGISTRATION NUMBER: 20,736
REFERENCE/DOCKET NUMBER: UGON/137/US
TELEPHONE: (860)527-9211
TELEFAX: (860)527-5029
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2265 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 35..1642
US-08-940-332-1

Query Match 68.2%; Score 2106.8; DB 2; Length 2265;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2111; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 175 GCTGGCTACATGGTGAACAGTGGAGAAATGGGAGATAAACAATTGAGGAGCTGAAGAA 234
DB |||||
QY 148 GCTGGCTACATGGTGAACAGTGGAGAAATGGGAGATAAACAATTGAGGAGCTGAAGAA 207
DB |||||
QY 235 AAATCTGGAGTACACAGCTTCTCTGCTGAGAGCCGCTTACATAGATGAGACACGGCAAT 294
DB |||||
QY 208 AAATCTGGAGTACACAGCTTCTCTGCTGAGAGCCGCTTACATAGATGAGACACGGCAAT 267
DB |||||
QY 295 CTGGACACGGAGGACGAGCTGACAGAGCTGCGGTTCAGATGCCGTTCGGAGGTGCG 354
DB |||||
QY 268 CTGGACACGGAGGACGAGCTGACAGAGCTGCGGTTCAGATGCCGTTCAGAGGTGCG 327
DB |||||
QY 355 GGAAGTGGCTCCACCTTACCCAGCAGCCGCGGCCAAAGCCGCGCCGAGCAGAGGA 414
DB |||||
QY 328 GGAAGTGGCTCCACCTTACCCAGCAGCCGCGGCCAAAGCCGCGCCGAGCAGAGGA 387
DB |||||
QY 415 GAAGCCCAAGTTCGGAACATGTGCACGCTGTGCAGGCTGGGATCTTCGTGGAACGGAT 474
DB |||||
QY 388 GAAGCCCAAGTTCGGAACATGTGCACGCTGTGCAGGCTGGGATCTTCGTGGAACGGAT 447
DB |||||
QY 475 GTTCCGGAGACATACAGCTCTGTGGGCCCACTTACTCTACTGCGGTCTCAACTGTCT 534
DB |||||
QY 448 GTTCCGGAGACATACAGCTCTGTGGGCCCACTTACTCTACTGCGGTCTCAACTGTCT 507
DB |||||
QY 535 CAAGAACCTGGATCTCTGCTGCTTGTGATGTCTTTTCTTGAACAGGACGAGATGACCA 594
DB |||||
QY 508 CAAGAACCTGGATCTCTGCTGCTTGTGATGTCTTTTCTTGAACAGGACGAGATGACCA 567
DB |||||
QY 595 TGCCCTGAGGACCATGTGTTTGTGATGTCTGACTCGGCATTAACCTCATCAGCCGCTCAA 654
DB |||||
QY 568 TGCCCTGAGGACCATGTGTTTGTGATGTCTGACTCGGCATTAACCTCATCAGCCGCTCAA 627
DB |||||
QY 655 GATTCCTCACTGTGTTTGTGATGTCTTCTGATGTCTTGTGAGACAGGCTATGGAAGTA 714
DB |||||
QY 628 GATTCCTCACTGTGTTTGTGATGTCTTCTGATGTCTTGTGAGACAGGCTATGGAAGTA 687
DB |||||
QY 715 CAAGAACCTTACCAACACAGATCCACGACGCGATGTTTACCCAGACAGTCATGCTT 774
DB |||||
QY 688 CAAGAACCTTACCAACACAGATCCACGACGCGATGTTTACCCAGACAGTCATGCTT 747
DB |||||
QY 775 CTTCCTCCGACAGGAGTGTGCTGCTGCTGAGATTTGAGCTTCCGCTCCGCTCACTCTT 834
DB |||||
QY 748 CTTCCTCCGACAGGAGTGTGCTGCTGCTGAGATTTGAGCTTCCGCTCCGCTCACTCTT 807
DB |||||
QY 835 TGCTGACGCTATCCATGATATGAGCAGCAGGCACTACCAACAGCTTCCACATCCAGAC 894
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QY 808 TGCTGACGCTATCCATGATATGAGCAGCAGGCACTACCAACAGCTTCCACATCCAGAC 867
DB |||||
QY 895 CAAATGACAATGTGCCATCGTGTACATGATCGTTCAGTGTGAGAAATCAACACATCAG 954
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QY 868 CAAATGACAATGTGCCATCGTGTACATGATCGTTCAGTGTGAGAAATCAACACATCAG 927
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QY 955 CTCTGTTTCCGATTTGATGACAGGATGATGAGATGAACATTTTCAACCTCACCAAGGA 1014
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QY 928 CTCTGTTTCCGATTTGATGACAGGATGATGAGATGAACATTTTCAACCTCACCAAGGA 987
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QY 1015 TGAGTTTGTAGAATCCGAGCCCTGGTCAATTGAGATGGTGTGGCCACAGACATGTCTTG 1074
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QY 988 TGAGTTTGTAGAATCCGAGCCCTGGTCAATTGAGATGGTGTGGCCACAGACATGTCTTG 1047
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QY 1075 CCAATTCCAGCAAGTGAAGACCATGAAGACAGCCCTTGCAACAGCTGGAGAGGATTGACAA 1134
DB |||||
QY 1048 CCAATTCCAGCAAGTGAAGACCATGAAGACAGCCCTTGCAACAGCTGGAGAGGATTGACAA 1107
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QY 1135 GCGCAAGGCCCTGTCTCTACTGCTCCATGCTGCTGACATCAGCCACCAACCAAGCAGTG 1194
DB |||||
QY 1108 GCGCAAGGCCCTGTCTCTACTGCTCCATGCTGCTGACATCAGCCACCAACCAAGCAGTG 1167
DB |||||
QY 1195 GTTGTGTCACAGCGTGTGGACCAAGGCCCTCATGAGGAATTTCTTCGTCAGGAGTACAA 1254
DB |||||
QY 1168 GTTGTGTCACAGCGTGTGGACCAAGGCCCTCATGAGGAATTTCTTCGTCAGGAGTACAA 1227
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QY 1255 GAGGCGAGAGTTGGGCGCTGCCCTTTCTCCACTCTGTGACCGCACTTCCACTCTAGTGGC 1314
DB |||||
QY 1228 GAGGCGAGAGTTGGGCGCTGCCCTTTCTCCACTCTGTGACCGCACTTCCACTCTAGTGGC 1287
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QY 1315 /CAGTCTCAGATAGGGTTCATCGACATTCATGTTGGAGCCACATTCCTCTGTGCTGACTGA 1374
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QY 1288 /CAGTCTCAGATAGGGTTCATCGACATTCATGTTGGAGCCACATTCCTCTGTGCTGACTGA 1347
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QY 1375 /GTGGCAGAGAAGAGTGTTCAGGCCCTTGGCGGATGAGGACTCCAAGTCTTAAAAACAGCC 1434
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QY 1348 /GTGGCAGAGAAGAGTGTTCAGGCCCTTGGCGGATGAGGACTCCAAGTCTTAAAAACAGCC 1407
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QY 1468 /GTGAGCTTTTCGTTTCCACCTTCAGCGCATTCAGGAGAAATGAAGCAAAATGGAAGGA 1527
DB |||||
QY 1555 /ACGGGACAGCAAGTGGCATCACCAACAGATGTCCATTGACGAGCTGTCCCCCTGTGAAGA 1614
DB |||||
QY 1528 /ACGGGACAGCAAGTGGCATCACCAACAGATGTCCATTGACGAGCTGTCCCCCTGTGAAGA 1587
DB |||||
QY 1615 /AGAGGCCCGCCCATCCCTCCGAAGATGAACAACACCAAGATGGAATCTGATTTAGCC 1674
DB |||||
QY 1588 /AGAGGCCCGCCCATCCCTCCGAAGATGAACAACCAAGATGGAATCTGATTTAGCC 1647
DB |||||
QY 1675 /CTGGGCTGCCAGAGTCTTCATTGATGCCAAAGTGTTCATGTCATCAGCACCATCCAT 1734
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QY 1648 /CTGGGCTGCCAGAGTCTTCATTGATGCCAAAGTGTTCATGTCATCAGCACCATCCAT 1707
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QY 1735 /CAGGACTGCTCCCGCATCTGCTCCAGGAGCGTGTGCTGGAAGAAACAACCCACCTG 1794
DB |||||
QY 1708 /CAGGACTGCTCCCGCATCTGCTCCAGGAGCGTGTGCTGGAAGAAACAACCCACCTG 1767
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QY 1795 /AAGGCCAAATGCGAGAGATTTGGGTTGGGGAAGGCGCCCTCCCGCTCCAGCACCAT 1854
DB |||||
QY 1768 /AAGGCCAAATGCGAGAGATTTGGGTTGGGGAAGGCGCCCTCCCGCTCCAGCACCAT 1827
DB |||||
QY 1855 /GGGTCGACTTAAATGTCGCGCAGCAAGCTCGGGAAGTTCAGGCTCCAGTCCAGTCACT 1914
DB |||||
QY 1828 /GGGTCGACTTAAATGTCGCGCAGCAAGCTCGGGAAGTTCAGGCTCCAGTCCAGTCACT 1887
DB |||||
QY 1915 /GTGCCATCCCTCAGGCTCTGGATTCCTTCATGGCCAGTGGCTGCCAGGAGCGGGA 1974
DB |||||
QY 1888 /GTGCCATCCCTCAGGCTCTGGATTCCTTCATGGCCAGTGGCTGCCAGGAGCGGGA 1947
DB |||||
QY 1975 /GTTCTCTGAGGCTTCCCGAGGCTTGGGAAGGGTTCAGAGTGCAGGCCCTGGGAGCC 2034
DB |||||
QY 1948 /GTTCTCTGAGGCTTCCCGAGGCTTGGGAAGGGTTCAGAGTGCAGGCCCTGGGAGCC 2007
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QY 2035 /TCCCGCATCCCTTTTGCCTCCAAAGTTTCTAAGCAATACATTTTGGGGGTTCCTCTCAGCCC 2094
DB |||||
QY 2008 /TCCCGCATCCCTTTTGCCTCCAAAGTTTCTAAGCAATACATTTTGGGGGTTCCTCTCAGCCC 2067
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QY 2095 /CCACCCCGAGATCTTAGCTGGCAGGCTGGGTGCCCTTTTCTCCCTGGGAGGGCTG 2154
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QY 2068 /CCACCCCGAGATCTTAGCTGGCAGGCTGGGTGCCCTTTTCTCCCTGGGAGGGCTG 2127
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QY 2155 /GAATAGATAGAAGCTGGGGTTTTCAGAGCCCTATGTTGGGAGGGGAGTGGATTC 2214
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QY 2128 /GAATAGATAGAAGCTGGGGTTTTCAGAGCCCTATGTTGGGAGGGGAGTGGATTC 2187
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QY 2215 /TTCAGGCACTGTGTACCTTTCTAGGATCTGGGAATGGGTGGGAGGACATCTCTTTCACC 2274
DB |||||
QY 2188 /TTCAGGCACTGTGTACCTTTCTAGGATCTGGGAATGGGTGGGAGGACATCTCTTTCACC 2247
DB |||||
QY 2275 /CCAGAAATGGCTGCTTC 2292
DB |||||
QY 2246 /CCAGAAATGGGGAATTC 2265
DB |||||

RESULT 2

US-07-872-644-26
: Sequence 26, Application US/07872644
: Patent No. 5389527
: GENERAL INFORMATION:
: APPLICANT: Beavo, Joseph A.
: APPLICANT: Bentley, Kelley
: APPLICANT: Charbonneau, Harry
: APPLICANT: Sonnenburg, William K.
: TITLE OF INVENTION: DNA Encoding Mammalian
: TITLE OF INVENTION: Phosphodiesterases
: NUMBER OF SEQUENCES: 58
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
: ADDRESSEE: Bicknell
: STREET: Two First National Plaza, 20 South Clark
: STREET: Street
: CITY: Chicago
: STATE: Illinois
: COUNTRY: USA
: ZIP: 60603
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/872,644
: FILING DATE: 19920420
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/688,356
: FILING DATE: 04-APR-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: No. 5389527and, Greta E.
: REGISTRATION NUMBER: 35,302
: REFERENCE/DOCKET NUMBER: 27866/30822
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (312) 346-5750
: TELEFAX: (312) 984-9740
: TELEX: 25-3856
: INFORMATION FOR SEQ ID NO: 26:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1844 base pairs
: TYPE: NUCLEIC ACID
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 114..1715
US-07-872-644-26

Query Match 43.6%; Score 1347.6; DB 1; Length 1844;

Best Local Similarity 90.6%; Pred. No. 0;
Matches 1473; Conservative 0; Mismatches 144; Indels 9; Gaps 3;

Qy	175	GCTCGCTACATGCTGAAGCAGTTGGAGATGGGGAGTAAACATTGAGGAGCTGAAGAA	234
Db	224	GCTCGCTACATGCTGAAGCAGTTGGAGATGGGGAGTAAACATTGAGGAGCTGAAGAA	283
Qy	235	AAATCTGGAGTACACAGCTTCTCTGCTGGAAGCCGCTACATAGATGAGACACGGCAAT	294
Db	284	AAACCTGGAGTACACAGCTTCTCTGCTGGAGCCGCTATATAGATGAGACTCGGCAAT	343
Qy	295	CTTGACACGAGGACGAGTGCAGAGCTGCGGTGCAGATGCCCTTCCGGAGGTGCG	354
Db	344	CCTGGACACGAGGATGAGTGCAGAGCTGCGGTCTGATGCGGTGCTTCAGAGGTGCG	403
Qy	355	GGACTGGCTGCCCTCCACCTTACCCAGCAGCCCGGGCCCAAGCCGCGGACGAGGA	414
Db	404	GGACTGGCTGCCCTCCACCTTACCCAGCAGCCCGGGCCCAAGCCGCGGAG---CGAAGA	460

Qy	415	GAAGCCCAAGTTCGAAAGCAATTGTGCACGCTGTGCAGGCTGGGATCTTCGTGGAAACGGAT	474
Db	461	GAAGCCCAAGTTCGGAAGCATCGTGCACGCGGTGCAGGCTGGCATCTTTGTGGAGCGGAT	520
Qy	475	GTTCGGAGAACATACACCTCTGTGGGCCCCACCTTACTCTACTCTGGGTTCCTCACTGTCT	534
Db	521	GTTCGGAGAACATACACCTCTGTGGGCCCCACCTTACTCTACTCTGGGTTCCTCACTGTCT	580
Qy	535	CAAGAACCTGGATCTCTGGTCTTTGATGTCTTTTCTTGAACACGAGCAGCAGATGACCA	594
Db	581	CAAGAACCTGGACCTTTGGTCTTTGATGTCTTTTCTTGAACCGGGCAGCAGATGACCA	640
Qy	595	TGCCCTGAGGACCAATGTTTTGATGTCTGTGACTCGGCATTAACCTCATCATGCCCTTCAA	654
Db	641	CGCCCTGAGGACCAATCGTTTTGAGCTGTCTGACTCGGCACAACTCATCATCAGCCGCTTAA	700
Qy	655	GATTCCTCCTGTTTTTTGATGAGTTTTCTGGATGCTTGGAGACAGGCTATGGGAAGTA	714
Db	701	GATTCCTCCTGTTTTTTGATGACTTTCTGGATGCTTGGAGACAGGCTATGGGAAGTA	760
Qy	715	CAAGAATCCTTACCACAAACAGATCCACGACGCGGATGTTTACCACAGCAGTCCATTGCTT	774
Db	761	CAAGAACCTTACCACAAACAGATCCACGACGCTGAGCTCACCCAGAGGCTCCACTGCTT	820
Qy	775	CTTGCTCCGACAGGATGCTGCTGCTCGGAGATTGAGTCTCTGGCCATCATCTT	834
Db	821	CTTGCTCCGACAGGATGCTGCTGCTCGGAGATTGAGTCTCTGGCCATCATCTT	880
Qy	835	TGCTGACAGTATCCATGATATGAGCAGACGGGCACTACCAACAGCTTCCACATCCAGAC	894
Db	881	TGCTGACAGGATCCACGACTATGAGCAGCTTGGCAGCTTCCACATCCAGAC	940
Qy	895	CAAGTCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	954
Db	941	CAATCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1000
Qy	955	CTCTGTTTCCGATTTGATGAGGATGATGAGATGAACATTTTCATCAACCTCACCAGGA	1014
Db	1001	CTCGTTTTCCGATTTGATGAGGATGATGAGATGAACATTTTCATCAACCTCACCAGGA	1060
Qy	1015	TGAGTTTGTAGAACTCCGAGCCCTGGTTCATTGAGATGGTGTGGCCACAGACATGCTCTG	1074
Db	1061	TGAGTTTGTAGAGCTCGGGCTCTGGTTCATTGAGATGGTGTGGCCACAGACATGCTCTG	1120
Qy	1075	CCATTTCAGCAAGTGAAGACCATGAAGACAGCCTTGAACAGCTTGGAGAGGATTGACAA	1134
Db	1121	CCATTTCAGCAAGTGAAGTCCATGAAGACAGCCTTGAACAGCTTGGAGAGGATTGACAA	1180
Qy	1135	GCCCAAGGCCCTGCTCTCTACTGCTCCATGCTGCTGACATGACATGACATGACATGACATG	1194
Db	1181	GTCCAAGGCCCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1240
Qy	1195	GTTGGTCCACAGCCGTTGGACCAAGGCCCTCATGGAGGAATTTCTTCCGTAGGGTGACAA	1254
Db	1241	GTCGTTTTCACAGCCGCTGGACCAAGGCCCTCATGGAGGAATTTCTTCCGCCAGGGTGACAA	1300
Qy	1255	GGAGCAGAGTTGGCCCTGCT	1314
Db	1301	GGAGCAGAGTTGGCCCTGCT	1360
Qy	1315	ACAGTCTCAGATAGGGTTTCATCGACTTTCATTTGTGGAGCCCACTTCTCTGCTGACTGA	1374
Db	1361	GCAGTCCAGATTTGTTTTCATCGACTTTCATTTGTGGAGCCCACTTCTCTGCTGACTGA	1420
Qy	1375	CGTGGCAGAGAGAGTGTTCAGCCCTTGGCCGATGAGGAGCTTCCAGTCTTAAACACGACC	1434
Db	1421	TGTGGCTGAGAAAGTGTTCAGCCCACTGGGGAGCAGCAGCTTGAAGTCTTAAACACGACC	1480
Qy	1435	CAGCTTTCAGTGGCCGAGCCCTCTCTGATGTGGAGTGGAGAGCCCACTTCTGATGT	1494
Db	1481	CAGCTTTCAGTGGCCGAGCCCTCTCTGATGTGGAGTGGAGAGCCCACTTCTGATGT	1540
Qy	1495	GGTCAGCTTTCTGTTCCACCTGGGTCAAGCGCATTCAGGAGAAATAGCAGAAATGGAAGGA	1554

Db 1541 GGTGAGTCTCCCTCCACTGGACCAATATACATTCAGGAGAACAGCAGAAATGAAGGA 1600
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Db 1601 ACGGGCGGCGAGCGCATCAACACAGATGTCATTCAGGAGTGTCCCTGTGAAGA 1660
QY 1615 AGAGGCGGCGGAGCGCATCAACACAGATGTCATTCAGGAGTGTCCCTGTGAAGA 1674
Db 1661 AGAGGCGGCGGAGCGCATCAACACAGATGTCATTCAGGAGTGTCCCTGTGAAGA 1719
QY 1675 CTGGGCTGGCGGAGTGTCTTCTGAGTCCAAAGTGTGATGTCATCAGCAGCATCCAT 1734
Db 1720 --GGGCTGGCGGAGTGTCTTCTGAGTCCAAAGTGTGATGTCATCAGCAGCATCCAT 1777
QY 1735 CAGGAGTGGCTGGCGGAGTGTCTTCTGAGTCCAAAGTGTGATGTCATCAGCAGCATCCAT 1791
Db 1778 CAGGAGTGGCTGGCGGAGTGTCTTCTGAGTCCAAAGTGTGATGTCATCAGCAGCATCCAT 1837
QY 1792 CTGAAG 1797
Db 1838 CCGAAG 1843

RESULT 3

US-08-297-494-26
; Sequence 26, Application US/08297494
; Patent No. 5580771
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/297,494
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 558077land, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1844 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:

; NAME/KEY: CDS
; LOCATION: 114..1715
; US-08-297-494-26
Query Match 43.6%; Score 1347.6; DB 1; Length 1844;
Best Local Similarity 90.6%; Pred. No. 0;
Matches 1473; Conservative 0; Mismatches 144; Indels 9; Gaps 3;
QY 175 GCTGCGGTACATGCTGAAGCAGTTGGAGATGGGAGATTAACATTTGAGGAGCTGAAGA 234
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QY 235 AAATCTGGAGTACACAGCTTCTCTGCTGGAAAGCGCTCTACATAGATGAGACACGGCAAT 294
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QY 295 CTGGGACACGAGGAGGAGCTGCAGGAGCTGCGGTGAGATGCGCTGCTGGAGGTGCG 354
Db 344 CTGGGACACGAGGAGGAGCTGCAGGAGCTGCGGTGAGATGCGGTGCTGATGCGGTGCG 403
QY 355 GAGTGGCTGGCTCCACCTTCCACCGAGGCGCGGCGCAAGGCGCGGCGGAGGAGGAG 414
Db 404 GAGTGGCTGGCTCCACCTTCCACCGAGGCGCGGCGCAAGGCGCGGAGGAGGAGGAG 460
QY 415 GAAGCCCAAGTTCGGAAGCATTTGTCACGCTGTGAGGCTGGGATCTTCTGCGAAGCGGAT 474
Db 461 GAAGCCCAAGTTCGGAAGCATTTGTCACGCTGTGAGGCTGGGATCTTCTGCGAAGCGGAT 520
QY 475 GTTCGGGAGNACATACACCTCTGTGGGCGGCGCTTACTCTACTGCGGTCTCAACTGCT 534
Db 521 GTTCGGGAGNACATACACCTCTGTGGGCGGCGCTTACTCTACTGCGGTCTCAACTGCT 580
QY 535 CAAGAACCTGGATCTCTGCTGCTTGTGATGCTTCTTGTGACCGGAGGAGGAGGAGGAG 594
Db 581 CAAGAACCTGGATCTCTGCTGCTTGTGATGCTTCTTGTGACCGGAGGAGGAGGAGGAG 640
QY 595 TGCCCTGAGGACCATTTGTTGAGTGTGCTGCTGCGCATAACTCATCAGCGCGCTTCAA 654
Db 641 CGCCCTGAGGACCATTTGTTGAGTGTGCTGCTGCGCATAACTCATCAGCGCGCTTCAA 700
QY 655 GATTCCACCTGCTTTTGTGATGATGCTTCTGCGATGCTTGGAGACAGGCTATGGGAAGA 714
Db 701 GATTCCACCTGCTTTTGTGATGATGCTTCTGCGATGCTTGGAGACAGGCTATGGGAAGA 760
QY 715 CAAGAACTCTTACCACAAACAGATCCACGCGGATGTTACCCAGACAGATCCATTCCTT 774
Db 761 CAAGAACTCTTACCACAAACAGATCCACGCGGATGTTACCCAGACAGATCCATTCCTT 820
QY 775 CTGCTCCGACAGGAGTGTGCTGCTGCTGCGGAGATTTGAGCTCCTGCGCATCATCTT 834
Db 821 CTGCTCCGACAGGAGTGTGCTGCTGCTGCGGAGATTTGAGCTCCTGCGCATCATCTT 880
QY 835 TGCTGAGCTATCCATGATTTATGAGCACACGCGGCTACCAACAGCTTCCACATCCAGAC 894
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QY 895 CAAGTCAGAAATGGCCATCGTGTACAAATGATGCTTCCAGTCTGCGGAGAAATCCACATCAG 954
Db 941 CAATCGAAATGGCCATCGTGTACAAATGATGCTTCCAGTCTGCGGAGAAATCCACATCAG 1000
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QY 1015 TGAGTTTGTAGACTCCGAGCCCTGCTGATGATGATGATGATGATGATGATGATGATGATG 1074
Db 1061 TGAGTTTGTAGACTCCGAGCCCTGCTGATGATGATGATGATGATGATGATGATGATGATG 1120
QY 1075 CCATTTCCAGAGTGAAGACCATTAAGACACGCTTGAACAGCTTGAACAGCTTGAACAG 1134
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Db 1181 GTCCAAAGCCCTCTCTGCTGCTCATGCTGCTGACATCAGCCACCACCACCAAGCAGTG 1240
QY 1195 GTTGGTCCACAGCGGTTGGACCAAGGCCCTCATGAGGAATCTTCCGTGAGGTGACAA 1254
Db 1241 GTCGGTTCCAGCGCGTGGACCAAGGCCCTCATGAGGAATCTTCCGCCAGGTGACAA 1300
QY 1255 GGAGCGAGTGGGCGCTGCGCTTTTCFCCACTCTGTACCGCACTTCCACTCTAGTGGC 1314
Db 1301 GGAGCTGAGCTGGCGCTGCGCTTTTCFCCACTCTGTACCGCACTTCCACTCTAGTGGC 1360
QY 1315 ACAGTCTCAGATAGGTTTCATGACTTCATTTGTGGAGCCACATTTCTGTGCTGACTGA 1374
Db 1361 CGAGTCCAGATAGGTTTCATGACTTCATTTGTGGAGCCACGTTCTGTGCTGCTACCGA 1420
QY 1375 CGTGCAGAGAGAGTGTTCAGCCCTTTCFCCACTCTGTACCGCACTTCCACTCTAGTGGC 1434
Db 1421 TGTGCTGAGAGAGTGTTCAGCCCTTTCFCCACTCTGTACCGCACTTCCACTCTAGTGGC 1480
QY 1435 CAGCTTTTCAGTGGCGCCAGCCCTCTCTGATGTGGAAGTGGAGACCCCAACCTGTATGT 1494
Db 1481 CAGCTTCCAGTGGCGCCAGCCCTCTCTGATGTGGAAGTGGAGACCCCAACCTGTATGT 1540
QY 1495 GGTGAGCTTTGTTCCAGCTGGTCAAGCGCATTCAGGAGATTAAGCAGAAATGAAGGA 1554
Db 1541 GGTGAGCTTTGTTCCAGCTGGTCAAGCGCATTCAGGAGATTAAGCAGAAATGAAGGA 1600
QY 1555 ACGGCGACAGAGTGTTCAGCCCTTTCFCCACTCTGTACCGCACTTCCACTCTAGTGGC 1614
Db 1601 ACGGCGGAGAGTGTTCAGCCCTTTCFCCACTCTGTACCGCACTTCCACTCTAGTGGC 1660
QY 1615 AGAGGCCCGCCATCCCTGCGGAGATGAACAAACAGAGTGGAGATCTGGATAGCC 1674
Db 1661 AGAGGCCCGCCATCCCTGCGGAGATGAACAAACAGAGTGGAGATCTGGATAGCC 1719
QY 1675 CTGGGCTGGCGCCAGGTTCTCATGAGTCCAAAGTGTGTTGATGATCATCAGCACCATCCAT 1734
Db 1720 --GGGGCTGGCGCCAGGTTCTCATGAGTCCAAAGTGTGTTGATGATCATCAGCACCATCCAT 1777
QY 1735 CAGGACTGGCTCCCGCATCTGCTCAAGGAGCGG ---GTCGTGGAAGAACACCCAC 1791
Db 1778 CGGACTGGCTCCCGCATCTGCTCGAGGGCGAATGGATGTCAAGGAACAGAAACCCAC 1837
QY 1792 CTGAAG 1797
Db 1838 CCGAAG 1843

RESULT 4

US-08-297-510-26
Sequence 26, Application US/08297510
Patent No. 5602019

GENERAL INFORMATION:

APPLICANT: Beavo, Joseph A.
APPLICANT: Bentley, Kelley
APPLICANT: Charbonneau, Harry
APPLICANT: Sonnenburg, William K.
TITLE OF INVENTION: DNA Encoding Mammalian
TITLE OF INVENTION: Phosphodiesterases
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/297,510
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/688,356
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5602019and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30822
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 1844 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 114..1715
US-08-297-510-26

Query Match 43.6%; Score 1347.6; DB 1; Length 1844;
Best Local Similarity 90.6%; Pred. No. 0;
Matches 1473; Conservative 0; Mismatches 144; Indels 9; Gaps 3;

QY 175 GCTGGCTTACATGGTGAAGCAGTGTGGAGATGGGAGATAAATTTGAGGAGCTCAAGAA 234
Db 224 GCTGGCTTACATGGTGAAGCAGTGTGGAGATGGGAGATAAATTTGAGGAGCTCAAGAA 283
QY 235 AAATCTGGAGTACACAGCTTCTCTCTGGAAGCCGCTTACATAGATGAGACACGGCAAT 294
Db 284 AAACCTGGAGTACACAGCTTCTCTCTGGAAGCCGCTTATATAGATGAGACTCGCAAT 343
QY 295 CTTGGACACGAGGAGAGCTGCGAGAGCTGCGGTCAGATGCCGTGCTTGGAGGTGG 354
Db 344 CTTGGACACGAGGAGAGCTGCGAGAGCTGCGGTCAGATGCCGTGCTTGGAGGTGG 403
QY 355 GAGTGGCTGGCTCCACCTTCCACCCAGCAGCCGCGCAAGCCGCGAGCAGAGA 414
Db 404 GAGTGGCTGGCTCCACCTTCCACCCAGCAGCCGCGCGCAAGCCGCGAG ---CGAGA 460
QY 415 GAAGCCCAAGTTCGGAAGCATTTGTCACGCTGTGCAAGGTGGAGTGGATTTGGTGGACGGAT 474
Db 461 GAAGCCCAAGTTCGGAAGCATTTGTCACGCTGTGCAAGGTGGAGTGGATTTGGTGGACGGAT 520
QY 475 GTTCCGGAGACATACACCTCTGTGGGCCCCCACTTACTTACTGCGGTCTCAACTGTCT 534
Db 521 GTTCCGGAGACATACACCTCTGTGGGCCCCCACTTACTTACTGCGGTCTCAACTGTCT 580
QY 535 CAAGAACCTGGATCTCTGCTTGTGATGCTCTTTTCCCTTGAACACGAGGACAGATGACCA 594
Db 581 CAAGAACCTGGACCTTTGGTGGCTTGTGATGCTCTTTTCCCTTGAACACGAGGACAGATGACCA 640
QY 595 TGCCCTGAGGACCATTTGTTTGTAGTGTGCTGACTCGGCAATAACCTCATCAGCGGTTCAA 654
Db 641 CGCCCTGAGGACCATCGTTTTTGTAGTGTGCTGACTCGGCAATAACCTCATCAGCGGTTCAA 700
QY 655 GATTCCTGCTGTTTTTGTAGTGTGCTGACTCGGCAATAACCTCATCAGCGGTTCAA 714
Db 701 GATTCCTGCTGTTTTTGTAGTGTGCTGACTCGGCAATAACCTCATCAGCGGTTCAA 760
QY 715 CAAGAATCTTACCACACAGATCCACGACCGCATGTTACCCAGACAGATGCTTGTCT 774
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QY 775 CTTGTCGCGACAGGAGTGGTGCACCTGCTGCGAGATTTGAGCTCTCGGCAATCATCTT 834

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Db 821 CTTGCTCCGACAGAGGATGGTCACTGCTGCGAGATGTAGGTCCTGGCCATCATCTT 880
Qy TGTGTCAGCTATCCATGATTATGAGCACACGGGCACTACCAACAGCTTCCACATCCAGC 894
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Qy 895 CAACTGAGATGTGCCATCGCTGACAAATGATCGTTTCAGTGTGGAGAAATCACCATCAG 954
Db 941 CAAATCGGAATGGCCATCTCTACAAAGACCGCTCAGTGTGGAGAAATCACCATCAG 1000
Qy 955 CTCTGTTTCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1014
Db 1001 CTCGGTTTCCGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1060
Qy 1015 TGAGTTTGTAGAACCTCCAGGCTGTCATGATGATGATGATGATGATGATGATGATG 1074
Db 1061 TGAATTTGTAGAGCTGGGCTGCTGATGATGATGATGATGATGATGATGATGATG 1120
Qy 1075 CCATTTCCAGCAAGTGAAGACCATGAAGACACCTTGAACACGCTGGAGAGATTGACAA 1134
Db 1121 CCATTTCCAGCAAGTGAAGTCCATGAAGACACCTTGAACACGCTGGAGAGATTGACAA 1180
Qy 1135 GCCAAGGCTTGTCTACTGCTCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1194
Db 1181 GTCCAAGGCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1240
Qy 1195 GTGTGTCACAGCCGTTGACCAAGCCCTCATGAGGAAATTTCTCCGTCAGGCTGACAA 1254
Db 1241 GTCGGTTTCACAGCCGCTGGACCAAGCCCTCATGAGGAAATTTCTCCGTCAGGCTGACAA 1300
Qy 1255 GGAGGCGAGTGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1314
Db 1301 GGAGGCGAGTGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1360
Qy 1315 ACAGTCTCAGATAGGCTTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1374
Db 1361 GCAGTCCCAAGATTGGTTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1420
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Db 1421 TGTGGCTGAGAAGTGTTCAGCCCTTGGCGATGAGGACTCCCAAGTCTAAACACCGCC 1480
Qy 1435 CAGCTTTCAGTGGCGCCAGCTCTCTGATGTGGAAGTGGAGACCCCAACCTCTGATGT 1494
Db 1481 CAGCTTTCAGTGGCGCCAGCTCTCTGATGTGGAAGTGGAGACCCCAACCTCTGATGT 1540
Qy 1495 GCTCAGCTTCTGCTCCAGCTGGTCAAGCGATTCAGGAGATTCAGGAGAAATGGAAGA 1554
Db 1541 GGTGAGCTTCCCTCCCTGACCAATATCATGAGGACACAGGAGAAATGGAAGA 1600
Qy 1555 ACGGCGAGCAAGTGGCATCACCAACAGATGTCATTCAGGAGTGTCCCTCTGGAAGA 1614
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Qy 1615 AGAGGCGCCCATCCCTGGCGAAGATGAACACCAAGATGGGAATCTGGATTAGCC 1674
Db 1661 AGAGGCGCCCATCCCTGGCGAAGATGAACACCAAGATGGGAATCTGGATTAGCC 1719
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Db 1720 --GGGCTGGCCAGGCTTTCATGAGTCCAAAGTGTGATGTCATCAGCAGCATCCAT 1777
Qy 1735 CAGGACTGGCTCCCATCTGCTCCAGGAGCGCTG---GTCTGGGAAGAAACACCCAC 1791
Db 1778 CAGGACTGGCTCCCATCTGCTCCAGGAGCGCTG---GTCTGGGAAGAAACACCCAC 1837
Qy 1792 CTGAAG 1797
Db 1838 CCGAAG 1843
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RESULT 5

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US-08-479-532-26
; Sequence 26, Application US/08479532
; Patent No. 5776752
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; TITLE OF INVENTION: Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESS: Marshall, O'Toole, Gerstein, Murray &
; ADDRESS: Blackwell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,532
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/297,494
; FILING DATE:
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5776752and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ. ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1844 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 114..1715
; US-08-479-532-26
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Query Match 43.6%; Score 1347.6; DB 1; Length 1844;
Best Local Similarity 90.6%; Pred. No. 0;
Matches 1473; Conservative 0; Mismatches 144; Indels 9; Gaps 3;

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Qy 175 GCTGCGCTACATGCTGAAGCAGTTGGAGATGGGAGATAAACATTGAGGAGCTGAAGAA 234
Db 224 GCTGCGCTACATGCTGAAGCAGTTGGAGAACGGGAGGTAACATTGAGGAGCTGAAGAA 283
Qy 235 AAATCTGGAGTACACAGCTTCTCTGCTGGAAGCCGCTACATAGATGAGACGCGCAAT 294
Db 284 AAACCTGGAGTACACAGCTTCTCTGCTGGAGGCCGCTATATAGATGAGACTCGGCAAT 343
Qy 295 CTTGGACACGGAGGAGCTGCGAGGCTGCGGCTCAGATCGGCTCCCTTCGGAGCTCG 354
Db 344 CTTGGACACGGAGGATGAGCTGCGAGGCTGCGGCTCAGATCGGCTCCCTTCAGAGTGG 403
Qy 355 GGAATGGCTGGCTCCACCTTACCCAGGAGCCCGGCGCAAGGCCGCGGAGCAGGA 414
Db 404 GGAATGGCTGGCTCCACCTTACCCAGGAGCCCGGCGCAAGGCCGCGGAGCAGGA 460
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QY 415 GAAGCCCAAGTTCCGAAGCATTTGTCACGCTGTGACGCTGGGATCTTCTGTTGGAACGGAT 474
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QY 475 GTTCCGGAGAACATACACCTCTGTGGGCCCCACCTTACTCTACTGGGGTTCTCAACTGTCT 534
Db 521 GTTCCGGAGAACATACACCTCTGTGGGCCCCACCTTACTCTACTGGGGTTCTCAACTGTCT 580
QY 535 CAAGAACCTGGATCTCTGCTGCTTTGTATGCTTTTCTTGAACAGGCGAGATGACCA 594
Db 581 CAAGAACCTGGATCTCTGCTGCTTTGTATGCTTTTCTTGAACAGGCGAGATGACCA 640
QY 595 TGCCCTGAGGACCAATTTGTTTGTAGTTGCTGACTGGCATACCTCTATCAGCCGCTTCAA 654
Db 641 CGCCCTGAGGACCAATTTGTTTGTAGTTGCTGACTGGCATACCTCTATCAGCCGCTTCAA 700
QY 655 GATTCCTCACTGTGTTTGTAGTTGCTGACTGGCATACCTCTATCAGCCGCTTCAA 714
Db 701 GATTCCTCACTGTGTTTGTAGTTGCTGACTGGCATACCTCTATCAGCCGCTTCAA 760
QY 715 CAAGAACCTTTACCAACACAGATCCAGCGACCGATGTTTACCCAGACAGTCCATTCCTT 774
Db 761 CAAGAACCTTTACCAACACAGATCCAGCGACCGATGTTTACCCAGACAGTCCATTCCTT 820
QY 775 CTGCTCCGACAGGATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 834
Db 821 CTGCTCCGACAGGATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 880
QY 835 TGCTGCACTATCATGATGATGACGACAGGCGACTACCAACAGCTTCCACATCCAGAC 894
Db 881 TGCTGCACTATCATGATGATGACGACAGGCGACTACCAACAGCTTCCACATCCAGAC 940
QY 895 CAAGTCAGAAATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATG 954
Db 941 CAAGTCAGAAATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATG 1000
QY 955 CTCTGTTTCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1014
Db 1001 CTCTGTTTCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1060
QY 1015 TGAGTTTGTAGAACTCCAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1074
Db 1061 TGAGTTTGTAGAACTCCAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1120
QY 1075 CCATTTCCAGAAAGTGAAGACCATGAAGACAGCCTTGAACAGCTGGAGAGATTGACAA 1134
Db 1121 CCATTTCCAGAAAGTGAAGACCATGAAGACAGCCTTGAACAGCTGGAGAGATTGACAA 1180
QY 1135 GCGCAAGCCCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1194
Db 1181 GCGCAAGCCCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1240
QY 1195 GTTGGTCCAGAGCGTTGGACAGGCGCTCATGAGGAAATTTCTTCCGTCAGGGTGACAA 1254
Db 1241 GTTGGTCCAGAGCGTTGGACAGGCGCTCATGAGGAAATTTCTTCCGTCAGGGTGACAA 1300
QY 1255 GGAGGACAGTTGGGCGCTGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1314
Db 1301 GGAGGACAGTTGGGCGCTGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1360
QY 1315 ACAGTCTCAGATAGGTTTCATCGACTTCATTTGAGGCGCCATTTCTTCTGCTGCTGCTGCTG 1374
Db 1361 ACAGTCTCAGATAGGTTTCATCGACTTCATTTGAGGCGCCATTTCTTCTGCTGCTGCTGCTG 1420
QY 1375 CGTGCGAGAGAGTGTTCAGCCCTTGGCGGATGAGAGTCCAGTCTAAAGTCTAAAGTCTAA 1434
Db 1421 TGTGCTGAGAGAGTGTTCAGCCCTTGGCGGATGAGAGTCCAGTCTAAAGTCTAAAGTCTAA 1480
QY 1435 CAGCTTTTCAGTGGGCGCCAGCTTCTCTGATGTTGGAAGTGGAGACCCACCTCTGATGT 1494
Db 1481 CAGCTTTTCAGTGGGCGCCAGCTTCTCTGATGTTGGAAGTGGAGACCCACCTCTGATGT 1540

RESULT 6

US-08-455-526-26
; Sequence 26, Application US/08455526
; Patent No. 5789553
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; TITLE OF INVENTION: Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/455,526
; FILING DATE: 31-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/297,494
; FILING DATE: 29-AUG-1994
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5789553and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1844 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

	Query Match	43.6%; Score 1347.6; DB 1; Length 1844;	
	Best Local Similarity	90.6%; pred. No. 0;	
	Matches 1473; Conservative	0; Mismatches 144; Indels	9; Gaps 3;
QY	175	GCTCGCTACATGTTGAAGCAGATTGGAGAATAAACAATTGAGAGACTGAAGAA	234
DB	224	GCTCGCTACATGTTGAAGCAGTTGGAGAAGCGGAGGTAAACAATTGAGAGACTGAAGAA	283
QY	235	AAATTCGAGTACACAGTCTCTGCTGGAAAGCCGCTCATAGATGAGACACGCCAAAT	294
DB	284	AAACTCGAGTACACAGTCTCTGCTGGAGGCCGCTATATAGATGAGACTCGGCNAAT	343
QY	295	CTTGACACCGGAGCACGAGCTGCAAGAGCTGCGGTAGATGCCGTGCTCTTGGAGGTGCG	354
DB	344	CCTGACACCGGAGGATGAGCTGCAAGAGCTGCGGTGCTGATCGGTGCTCTCAGAGTGGC	403
QY	355	GGACTGGCTGCGCTCCACGCTTCAACCACAGACGGCCCGGCCAAAGGCCGCCGACAGGAA	414
DB	404	GGACTGGCTGCGCTCCACGCTTCAACCACAGACGCCGCCGCGCCNAGGCCGAG--CGAAGA	460
QY	415	GGAAGCCCAGTTCCGAAGCATATGTGCAGCGTGTGCAGGCTGGAGTCTCTGTGGNACGGAT	474
DB	461	GGAAGCCCAGTTCCGAGCATCTGTGCACGCGGTGCAGCTGGCATCTTGTGGAGCGGAT	520
QY	475	GTTCCGGAGAACATACACCTCTGTGGGCCGCCCACTACTCTACTCGGTTCTCAAACCTGCT	534
DB	521	GTTCCGGAGAACGTAACCTCTGTGGGCCGCCCACTACTCTCAACTCGCTCTCAAACCTGCT	580
QY	535	CAAGAACTGGATCTGTGTTGTGTGTCTTTTCTTGAACACAGGCGACAGATGACCA	594
DB	581	CAAGAACTGGACCTTGGTGTGTGTCTTTCTTGAACCGGGCAGCAGATGACCA	640
QY	595	TGCGCTGAGGACCAATGTTTTGAGTTGCTGCTACTCGGCATAACCTCAATCAAGCCGTTCAA	654
DB	641	CGCCCTGAGGACCAATGTTTTGAGTTGAGTCTGCTACTCGGCACACACCTCAATCAAGCCGTTAA	700
QY	655	GATTCACCATGTGTTTTGATGAGTTTCTCGATGCTTGGAGACAGGCTATGGGAAGTA	714
DB	701	GATTCACCATGTGTTTTGATGACTTCTCGATGCTTGGAGACAGGCTATGGGAAGTA	760
QY	715	CAAGAACTCTTACCACAAACAGATCCACAGCCGATGTACCCAGACAGTCAATTCGTT	774
DB	761	CAAGAACTCTTACCACAAACAGATCCACAGCTGACGTCACCCAGACGCTCACTGCTT	820
QY	775	CTTGCTCCGCACAGGATGTTGACATGCTGTCGGAGATTGAGCTCTGGCCCATCATCTT	834
DB	821	CTTGCTCCGCACAGGATGTTGACATGCTGTCGGAGATTGAGCTCTGGCCCATCATCTT	880
QY	835	TGCTGTCAGCTATCCATGATTATGAGCACACGGGCATACCAACAGCTCCACATCCAGAC	894
DB	881	TGCTGTCAGOGATCCACGACATGAGACACATGGCATTACACAGCTCCACATCCAGAC	940
QY	895	CAAGTCAAGATGTGCCATCGTACAATGATGCTTCAGTCTGGAGAAATCACCAATCAG	954
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QY	955	CTCTGTTTTCCGATTGTATGTCAGGATGATGAGATGAACATTTTCATCAACTCACCAAGAA	1014
DB	1001	CTCGGTTTTCCGAATGATGACGAGACGAGATGAACATTTTCATCAACTCACCAAGAA	1060
QY	1015	TGAGTTGTAGAACTCCGAGCCCTGGTTCANTTAGATGGTGTGGCCACAGACATGTCCTG	1074
DB	1061	TGAGTTGTAGAGCTCGGGCTCTGGTTCATTTAGATGGTGTGGCCACAGACATGTCCTG	1120
QY	1075	CCATTTCCGAAGTGAAGACCATGAAGACAGCTTGCACACCTCGAGAGGATTCACAA	1134

RESULT 7
 US-08-455-525-26
 US-08-455-525-26
 Sequence No. 5800987
 GENERAL INFORMATION:
 APPLICANT: Beavo, Joseph A.
 APPLICANT: Bentley, Kelley
 APPLICANT: Charbonneau, William K
 APPLICANT: Charbonneau, William K
 APPLICANT: INVENTION: DNA Encoding
 TITLE OF INVENTION: Phosphodiester
 NUMBER OF SEQUENCES: 58
 CORRESPONDENCE ADDRESS:
 ADDRESS: Marshall, O'Toole,
 ADDRESS: Backnell
 STREET: Two First National Plaza
 STREET: Street
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60603
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

Query Match 43.6%; Score 1347.6; DB 1; Length 1844;

QY	175	GCTGCGCTACATGGTGAAGCAGTTTGGAGAATTGGGAGATAAACATTTGAGGAGCTGAAGAA	234
DB	224	GCTGCGCTACATGGTGAAGCAGTTTGGAGAACGGGAGGTAACATTTGAGGAGCTGAAGAA	283
QY	235	AAATCTGGAGTACACACTTCTCTGCTGGAAAGCGTCTACATATAGATGAGACACGGCAAT	294
DB	284	AAACCTGGAGTACACACTTCTCTGCTGGAGCGGCTTATATAGATGAGACTTCGGCAAT	343
QY	295	CTTGGACACGGAGGACGAGTGCAGGAGCTCGGTCAGATCGGTCGCTTCGGAGGTCGG	354
DB	344	CTTGGACACGGAGGATGAGCTGCAAGAGCTCGGTCGTGATCGGTCGCTTCAGAGGTCGG	403
QY	355	GGACTGSGCTGGCCTCCACCTTCACCCAGCAGCGCCGGGCCAAAGGCCCGCCGAGCAGAGA	414
DB	404	GGACTGSGCTGGCCTCCACCTTCACCCAGCAGACCCGGGCCAAAGGCCCGAG--CGAAGA	460
QY	415	GAAGCCCAAGTTCGGAAGCATGTGTGCACGCTGTGCAGGCTGGGATCTTCGTGGAAACGGAT	474
DB	461	GAAGCCCAAGTTCGGGAGCATCGTGCACGCGGTGCAGGCTGGCATCTTTGTGGAGCGGAT	520
QY	475	GTTCGGGAGAACATACACCTCTGTGGGCCCCACTTACTCTACTGGGTTCTCAACTGCTCT	534
DB	521	GTTCGGGAGAACGTACACCTCTGTGGGCCCCACCTTACTTCCACTGCCGTCCTCAACTGCT	580
QY	535	CAAGAACTCGGATCTCTGGTGCTTTGATGTCTTTTCCTTGAACACAGGCAGCAGATGACCA	594
DB	581	CAAGAACTGGACCTTTGGTGCTTTTGATGTCTTTTCCTTGAACCGGGCAGCAGATGACCA	640
QY	595	TGCCCTTGAGGACCAATTTTTTGGAGTTGCTGACTCGGCATTAACCTCATCAGCCGCTTCAA	654
DB	641	CGCCCTTGAGGACCATGCTTTTGGAGCTGCTGACTCGGCACAACCTCATCAGCCGCTTCAA	700
QY	655	GATTCCCACTGTGTTTTTGATGAGTGTCTCCTGGATGCCCTTGAGACAGAGGCTATGGGAAGTA	714
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US-09-663-481-2.FBI

[illegible]

Db 1421 TGTGGCTGAGAAGAGTGTCCAGCCACCAGGGAGCAGACTCGAAGTCTAAAAACAGCC 1480
Qy 1435 CAGCTTTTCAGTGGCGCCAGCCCTCTCTGGATGTGGAAGTGGGAGACCCCAACCTGATGT 1494
Db 1481 CAGCTTCAGTGGCGCCAGCCCTCTCTGGATGTGGAAGTGGGAGACCCCAACCTGACGT 1540
Qy 1495 GGTGAGCTTTCTGTTCCACCTGGTCAAGCCGATTCAGGAGAATTAAGCAGAAATGGAAGGA 1554
Db 1541 GGTGAGCTTTCTGTTCCACCTGGTCAAGCCGATTCAGGAGAATTAAGCAGAAATGGAAGGA 1600
Qy 1555 ACGGGCAGCAGTGGGATCACCACACAGATGTCCATTCAGAGAGTGTCCCTCTGTGAAGA 1614
Db 1601 ACGGGCAGCAGTGGGATCACCACACAGATGTCCATTCAGAGAGTGTCCCTCTGTGAAGA 1660
Qy 1615 AGAGGCCCCCCTCCCTGCGGAAGATGAACCAACAGATGGGAATCTGGATTAGCC 1674
Db 1661 AGAGGCCCCCCTCCCTGCGGAAGATGAACCAACAGATGGGAATCTGGATTAGCC 1719
Qy 1675 CTGGGGCTGGCCCCAGGCTCTTCATTGAGTCCAAAGTGTTCATCAGCACCACCATCCAT 1734
Db 1720 -GGGGCTGGCCCCAGGCTCTTCATTGAGTCCAAAGTGTTCATCAGCACCACCATCCAT 1777
Qy 1735 CAGGACTGGCTCCCCATCTGCTCCAAAGGAGCGTG---GTGCGGGAAGAAACCCAC 1791
Db 1778 CGGGACTGGCTCCCCATCTGCTCCGAGGCGAATGATGTCAAGGAACAGAAACCCAC 1837
Qy 1792 CTGAAG 1797
Db 1838 CCGAAG 1843

RESULT 9

PCT-US92-03222-26
; Sequence 26, Application PC/TUS9203222
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; TITLE OF INVENTION: Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/03222
; FILING DATE: 19920420
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 26:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 1844 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 114..1715
; PCT-US92-03222-26

Query Match 43.6%; Score 1347.6; DB 5; Length 1844;
Best Local Similarity 90.6%; Pred. No. 0;
Matches 1473; Conservative 0; Mismatches 144; Indels 9; Gaps 3;

Qy 175 GCTCGCTACATGCTGAAGCAGTTGGAGATGGGAGATAAACAATTCAGGAGCTGAAGAA 234
Db 224 GCTCGCTACATGCTGAAGCAGTTGGAGATGGGAGATAAACAATTCAGGAGCTGAAGAA 283
Qy 235 AAATCTGGAGTACACAGCTTCTCTGCTGGAAGCCGCTTACATAGATGAGACACGCAAT 294
Db 284 AAACCTGGAGTACACAGCTTCTCTGCTGGAGCCGCTATATATAGATGAGACTCGCAAT 343
Qy 295 CTTGGACACGAGGAGCAGAGCTGCGAGAGCTGCGGTTCAGATGCCGTGCTTCGGAGGTGCG 354
Db 344 CTTGGACACGAGGAGTGAAGCTGCGAGAGCTGCGGTTCAGATGCCGTGCTTCAGAGGTGCG 403
Qy 355 GGACTGGCTGGCTTCCACCTTCACCCAGCAGGCCCGGGCCAAAGGCCCGCAGCAGGAA 414
Db 404 GGACTGGCTGGCTTCCACCTTCACCCAGCAGGCCCGGGCCAAAGGCCCGGAG---CGAAGA 460
Qy 415 GAAGCCCAAGTTCCGAAGCATTGTGCACGCTGTGCAGGCTGGGATCTTCGTGGAAACGAT 474
Db 461 GAAGCCCAAGTTCCGAAGCATTGTGCACGCTGTGCAGGCTGGGATCTTCGTGGAGCGAT 520
Qy 475 GTTCCGGAGAACATACACCTCTGTGGGCCCCACCTTACTTCTACTCGGTTCCTCAACTGTCT 534
Db 521 GTTCCGGAGAACATACACCTCTGTGGGCCCCACCTTACTTCTACTCGGTTCCTCAACTGTCT 580
Qy 535 CAAGAACCTGGATCTCTGGTGTCTTGTATGTCTTTCTTCCCTTGAACACGACGACGACGACCA 594
Db 581 CAAGAACCTGGATCTCTGGTGTCTTGTATGTCTTTCTTCCCTTGAACACGACGACGACGACCA 640
Qy 595 TGCCCTGAGGACCACTTGTCTTGTAGTGTCTGACTCGGCATTAACCTTCATCAGCCCTCAAA 654
Db 641 CGCCCTGAGGACCACTTGTCTTGTAGTGTCTGACTCGGCATTAACCTTCATCAGCCCTTAA 700
Qy 655 GATTCACCACTGTGTTTGTGATGATGTTCTTCCCTGGATGCTTGGAGACGCTATGGGAAGTA 714
Db 701 GATTCACCACTGTGTTTGTGATGATGTTCTTCCCTGGATGCTTGGAGACGCTATGGGAAGTA 760
Qy 715 CAAGAATCCTTACCACACACAGATGCCAGCAGCCGATGTTTACCCAGACAGTCCATTGCTT 774
Db 761 CAAGAATCCTTACCACACACAGATGCCAGCAGCCGATGTTTACCCAGACAGTCCATTGCTT 820
Qy 775 CTTGCTCCGACACAGGATGTTGCTGCTGCGAGATGAGCTTCCCTGGCCATCATCTT 834
Db 821 CTTGCTCCGACACAGGATGTTGCTGCTGCGAGATGAGCTTCCCTGGCCATCATCTT 880
Qy 835 TGCTGACGCTATCCATGATATGAGCAGACGCGGACCTACCAACAGCTTCCACATCCAGAC 894
Db 881 TGCTGACGCTATCCATGATATGAGCAGACCTTACCAACAGCTTCCACATCCAGAC 940
Qy 895 CAAGTCAGATGTCCTATGCTGTACATGATGCTTCACTGCTGAGAGATCACCACATCAG 954
Db 941 CAATCGGAATGCGCCATCTCTGTACAAACGACCCGCTAGTGTGGAGAAATCACCACATCAG 1000
Qy 955 CTCTGTTTCCGATTGATGAGGATGATGAGATCAACATTTTCATCAACCTTCACCAAGGA 1014
Db 1001 CTCTGTTTCCGATTGATGAGGATGATGAGATCAACATTTTCATCAACCTTCACCAAGGA 1060
Qy 1015 TGAGTTTGTAGAACTCCGAGCCCTGGTTCATTGAGATGGTGTGGCCACAGACATGCTCTG 1074

Db 782 AAGATCCCAATTTCTGCACTTGTCTCTATTTGTGAGGCGCTTGAAGTGGGATACAGCAAG 841
QY 713 TACAGAAATCTTACCAACACAGATCCACGCGCGATGTACCCACAGATCCATTCG 772
Db 842 CACAAAATCTTACCATAATTAATGACGCTCGCGATGTACACAGACAGTGCATTAC 901
QY 773 TTTCTGTCTCCGACAGGAGTGGTGCATCTGCTGCGAGATTTGAGCTCTCGCCATCATC 832
Db 902 CTCCTCTATAGACAGGAGTGGCGAATCTGCTGACGAGCTGGAGATCTTTGCTATATC 961
QY 833 TTTCTGTGAGTATCCATGATATGAGACACGCGGCTACCAACAGCTTCCACATCCAG 892
Db 962 TTTCTGAGTCCATCCATGATAGTACGATACCGGAACCAACAAATTTCCACATTCAG 1021
QY 893 ACCAAGTCAGATGTGCATCTGTACAAATGATCTGAGTCTGAGTCTGGGAATCCACATC 952
Db 1022 ACTCGGTGTATCCAGCTATTTCTGTATATACAGATCTGTACTGGAGATCCACATTTA 1081
QY 953 AGCTCTGTTTCCGATTTGATGACGAGTATGAG---ATGAACATTTTTCATCAACCTCAC 1009
Db 1082 AGTCAGCTTATCCCTTCTGCAAGATGACGAGGAATGATATTTGATTAACCTCTCA 1141
QY 1010 AAGATGAGTTGTAGAACTCCGAGCCCTGTCTATGAGATGTGTGGCCACAGACATG 1069
Db 1142 AAGGATGACTGGAGGAGTTTCGAACCTTGTGTAATTTGAAATGTTGATGGCCACAGATG 1201
QY 1070 TCCTGCAATTTCCAGCAAGTGAAGACCATGAGACGCTTGCAACAGCTGGAGGATT 1129
Db 1202 TCTTGTCACTTCCAAACAAATCAAGCAATGAAGACTGCTGTGACGAGCCAGAACCAAT 1261
QY 1130 GACAAGGCCAAGGCCCTGCTCTACTGCTCATGCTGTGACATCAGCCACCCCAACCAAG 1189
Db 1262 GAAAGCCAAAGCCCTTATCCCTTATGCTGATACAGCAGATATAGCCATCCAGCAAA 1321
QY 1190 CAGTGTGTGTCACAGCCGTTGGACCAAGCCCTCATGAGGAAATTTCCGTCAGGGT 1249
Db 1322 GCATGGGACCTTCCATCATCGTGTGACAAATGTCATCTCTGGAGGATTTCTTCAGACAGGGT 1381
QY 1250 GACAAGGAGGAGGAGTGGGCGCTGCTCTTCTCCACTCTGTGACCGCACCTTCACACTA 1309
Db 1382 GACAGAGNAGCAGAGCTGGGCGCTGCTTCTCTCTGCTGTGACCGNAGTCCACTATG 1441
QY 1310 GTGCAAGTCTCAGATAGGGTTTCATCGACTTATTTGAGAGCCACATTTCTGTGTGTG 1369
Db 1442 GTTCTCAGTCACAAGTAGGTTTCATTGATTTTCATCGTGGAAACCCACCTTCACCTGTGCT 1501
QY 1370 ACTGACGTGGCAGAGAGAGTGTTCAGCCCTGGCGGATGAGGACTCCAACTCT 1423
Db 1502 ACGGACATGACCGGAGAGATTTGTGAGTCCATTAATCGATGAAGACTCTCAAACT 1555

RESULT 11

US-08-297-494-50
; Sequence 50, Application US/08297494
; Patent No. 5580771

GENERAL INFORMATION:

; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; TITLE OF INVENTION: Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/297,494
; FILING DATE:

CLASSIFICATION: 435

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5580771and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 50:

SEQUENCE CHARACTERISTICS:

; LENGTH: 2693 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

FEATURE:

; NAME/KEY: CDS

; LOCATION: 176..2077

US-08-297-494-50

Query Match

Best Local Similarity 19.3%; Score 598; DB 1; Length 2693;

Matches 851; Conservative 0; Mismatches 400; Indels 3; Gaps 1;

QY 173 AGCTGCGCTACATGGTGAAGCAGTTGGAGAAATGGGGAGATAAACAATTGAGGAGCTGAAG 232
Db 302 AGATTACGGTCTTTGGTCAACAATTAGAGAGAGGGGAAGCTTCAGTGGTAGATCTTAAG 361
QY 233 AAAAATCTGGAGTACACAGCTTCTGCTGGAAGCCGCTACATAGATGACACAGCGCAA 292
Db 362 AAGAATTTGGAATATGACGCCACAGTGTGTTGAATCTGTGTATTTATGATGAACAAGGAGA 421
QY 293 ATCTTTGACACGGAGGACAGCTGCAGGAGCTGCGGTGAGATGCGCTGCGCTTCGAGGTG 352
Db 422 CTCCTGGATCAGAGGATGAGCTCAGTCAATTCAGTCAAGTGTGCTGCTTCTGAGGTC 481
QY 353 CGGAGCTGGCTGGCTTCCACCTTCACCCAGCAGCGCCGCGCCAAAGGCGCCGAGCAGAG 412
Db 482 CGAGACTGGCTGGCTTCCACCTTCACCGCGCAGATGGGAGTGTGCTCAGGAGGAGCGAC 541
QY 413 GAGAAGCCCAAGTTCCGAAGCATTGTGCACGCTGTGACGCTGGAGCTTCTGTCGAACGG 472
Db 542 GAGAAGCCCGGTTCAAGAGCATCGTTCACGCGCAGGCTGGAGTATTTGTGGAGAGA 601
QY 473 ATGTTCCGGAGAACAATACACCTCTGTGGGCCCCACTTACTCTACTGCGGTCTCAACTGT 532
Db 602 ATGATAGACGACATCAACATGTTGATGAGTATCCACAGCTGTTATTGAGGCA 661
QY 533 CTCAAGAACCTGGATCTCTGGTGTGTTGATGTCTTTTCCCTTTGAACACGAGCAGATGAC 592
Db 662 TTAAGGATGTGGCAAGTGTCTTTCACGCTCTTTTCCCTCAATGAGGCGCAGTGGGAT 721
QY 593 CATGCCCTGAGGACCATTTGTTTGTGAGTGTGCTGAGTCCGCAATACCTCATCAGCGGCTTC 652
Db 722 CATGACCTGAAATTTATTTTCTATGAACACTACTACACAGTATGATCTGATCAGCGGTTTC 781
QY 653 AAGATCCCACTGTTTGTGATGATGTTTCTGATGCTTGGAGAGCTGTTGGAGAGCTATGGGAG 712
Db 782 AAGATCCCACTTCTGCACTTGTCTCAATTTGTGGAGGCGCTTGGAGTGGGATACAGCAAG 841
QY 713 TACAAGATCCTTACCACAACAGATCCACGCGCGATGTTTACCCAGACAGTCCCATTCG 772

842 CACAAAATCCTTACCATAACTTAATGACGCTGCCGATGTTACACAGACAGTGCATTAC 901
773 TTCTTCTCGCCACAGAGGATGTCACCTGCTCGGAGATTGAGCTCTGTGGCCATCATC 832
902 CTCCTCTATAACAGAGGAGTGGCGAACTGGCTGACGGAGCTGGAGATCTTTGCTATAATC 961
833 TTGTGTGAGCTATCCATGATTATGACAGCAGGCTACTACCAACAGCTTCCACATCCAG 892
962 TTCTCAGCTGCCATCCATGACTACGAGCATACCGGAACCAACCAAAATTCACATTCAG 1021
893 ACCAATGAGATGTCGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 952
1022 ATCGGTCTGATCCAGCTATCTGTATATGATGATGATGATGATGATGATGATGATGATG 1081
953 AGCTCTGTTTCCGATGATGAGGATGAG---ATGAACATTTTCATCAACCTCAC 1009
1082 ATGCGAGCTTATCGGCTTCTGCAAGATGACGAGGAATGAATATTTGATTAACCTCA 1141
1010 AAGATGATGTTGTAGAACTCCGAGCCCTGGTCAATGATGATGATGATGATGATGATGATG 1069
1142 AAGATGATGATGAGGAGGATTCGAACCTTGGTAAATGATGATGATGATGATGATGATGATG 1201
1070 TCTGCTGATTTCCAGCAAGTGAAGACCATGAAGACAGCTTGCACAGCTGGAGAGGAT 1129
1202 TCTGTGCTATCCCAACAAATCAAGCAATGAGACTGCTGACAGCAGCCAGAGCCATT 1261
1130 GACAAAGCCCAAGCCCTGTCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1189
1262 GAAAGCCCAAGAGCTTATCCCTTATGCTGATACAGCAGATATTAAGCCATCCAGCAAAA 1321
1190 CAGTGTGTTGCTCAGAGCGGTTGGACCAAGGCGCTCATGGAGGAATTTCTCGTCAGGCT 1249
1322 GCATGGGACTCCATCATCGCTGGACAATGTCACTCTCGGAGGATTTCTCAGACAGGCT 1381
1250 GACAGGAGGAGGAGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1309
1382 GACAGAGAGAGAGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1441
1310 GTGACAGCTCAGATAGGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1369
1442 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1501
1370 ACTGAGTGGGAGAGAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1423
1502 ACGGACATGACGAGAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1555

RESULT 12

US-08-297-510-50
; Sequence 50, Application US/08297510
; Patent No. 5602019

GENERAL INFORMATION:

; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; TITLE OF INVENTION: Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESS: Marshall,
; ADDRESS: Bicknell,
; STREET: Two First National Plaza, 20 South Clark
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/297,510
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5602019and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/POCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2693 base pairs
; TYPE: nucleic acid
; STRANDELNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; NAME/KEY: CDS
; LOCATION: 176..2077
US-08-297-510-50

Query Match

Best Local Similarity 19.3%; Score 598; DB 1; Length 2693;

Matches 851; Conservative 0; Mismatches 400; Indels 3; Gaps 1;

Qy 173 AGGCTGGCTCATGCTGAACAGCTGGAGATGGAGATGAACATTTGAGAGCTGAAG 232
Db 302 AGATTACGCTCTTTGGTCAACAAATAGAGAGAGGAGGAGCTTCACTGGTAGATTAA 361
Qy 233 AAAATCTGGAGTACAGCTTCTCTGCTGAAGCCGCTACATAGATGACAGCGCAA 292
Db 362 AGAATTTGGAAATGACGACCACTGCTGATCTGTATATTTGATGAACAGGAGA 421
Qy 293 ATCTTGACACGAGGAGAGCTGACAGAGTGGGCTGAGATGCGGCTTCGAGGAGTG 352
Db 422 CTCCTGATACAGAGGATGAGCTCAGTGACATTCAGTCAATGCTGCTGCTTCTGAGGTC 481
Qy 353 CGGACTGGCTGGCTCCACCTTCCACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 412
Db 482 CGAGACTGGCTGGCTCCACCTTCCACGCGCAGATGGGAGTGTGCTCAGAGAGGAGG 541
Qy 413 GAGAGCCCAAGTTCCGAAGCATTTGTCAGCTGTCAGGCTGGGATCTTCGTGGAACGG 472
Db 542 GAGAGCCCGGTTCAAGAGCATCGTTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAG 601
Qy 473 ATGTTCCGGAGACATACACCTCTGTGGGCGCCACTTACTCTACTGCGGTTCTCAACTGT 532
Db 602 ATGTATAGACGAGCATCAACATGTTGGAGTGTGCTATCCACAGCTGTTATTGAGGCA 661
Qy 533 CTCAAGAACCTGGATCTCTGCTGCTTTGATGCTTTTCTTTGAAACAGGAGGAGGAGG 592
Db 662 TTAAGGATGAGCAAGTGGTCTCTTTGACGCTCTTTCCCTCAATGAGGCGAGTGGGAT 721
Qy 593 CATGCTCGAGGACCATTTTGTAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 652
Db 722 CATGCTGAAATTTTCTATGAACTACTACAGCTTATGATCTGATCAGCAGCGGTTTC 781
Qy 653 AGATTTCCGAGTGTGTTTGTGATGATTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 712
Db 782 PAGATCCCATTTCTGCAGTGTCTCATTTGTGGGCGCCCTGGAGTGGGATGAGCAG 841
Qy 713 TACAAGATCTTTACCAACAGGATCCAGAGCGGATGTTACCCAGAGCTCATGCTTC 772
Db 842 CACAAAATCTTTACCACTAATTAATGACGCTGCCGATGTTACAGAGAGCTCATATAC 901
Qy 773 TCTTGTCTCGCAGAGGATGGTGCATGCTGCTGCGAGATTTGAGCTCTCTGGCCATCATC 832

Db 902 CTCCTCTATAAGACAGAGAGTGGCGAAGCTGGCTACGGAGCTGGAGATCTTTGCTATAATC 961
QY TTTGCTGAGCTATCATGATTATGACGACAGCGGCACTACCAACAGCTTCCACATCCAG 892
Db TTTGCTGAGCTATCATGATTATGACGACAGCGGCACTACCAACAGCTTCCACATCCAG 1021
QY TTTGCTGAGCTATCATGATTATGACGACAGCGGCACTACCAACAGCTTCCACATCCAG 952
Db TTTGCTGAGCTATCATGATTATGACGACAGCGGCACTACCAACAGCTTCCACATCCAG 1081
QY TTTGCTGAGCTATCATGATTATGACGACAGCGGCACTACCAACAGCTTCCACATCCAG 1009
Db TTTGCTGAGCTATCATGATTATGACGACAGCGGCACTACCAACAGCTTCCACATCCAG 1141
QY TTTGCTGAGCTATCATGATTATGACGACAGCGGCACTACCAACAGCTTCCACATCCAG 1069
Db TTTGCTGAGCTATCATGATTATGACGACAGCGGCACTACCAACAGCTTCCACATCCAG 1201
QY TTTGCTGAGCTATCATGATTATGACGACAGCGGCACTACCAACAGCTTCCACATCCAG 1129
Db TTTGCTGAGCTATCATGATTATGACGACAGCGGCACTACCAACAGCTTCCACATCCAG 1261
QY TTTGCTGAGCTATCATGATTATGACGACAGCGGCACTACCAACAGCTTCCACATCCAG 1189
Db TTTGCTGAGCTATCATGATTATGACGACAGCGGCACTACCAACAGCTTCCACATCCAG 1321
QY TTTGCTGAGCTATCATGATTATGACGACAGCGGCACTACCAACAGCTTCCACATCCAG 1249
Db TTTGCTGAGCTATCATGATTATGACGACAGCGGCACTACCAACAGCTTCCACATCCAG 1381
QY TTTGCTGAGCTATCATGATTATGACGACAGCGGCACTACCAACAGCTTCCACATCCAG 1309
Db TTTGCTGAGCTATCATGATTATGACGACAGCGGCACTACCAACAGCTTCCACATCCAG 1441
QY TTTGCTGAGCTATCATGATTATGACGACAGCGGCACTACCAACAGCTTCCACATCCAG 1369
Db TTTGCTGAGCTATCATGATTATGACGACAGCGGCACTACCAACAGCTTCCACATCCAG 1501
QY TTTGCTGAGCTATCATGATTATGACGACAGCGGCACTACCAACAGCTTCCACATCCAG 1423
Db TTTGCTGAGCTATCATGATTATGACGACAGCGGCACTACCAACAGCTTCCACATCCAG 1555

RESULT 13

US-08-479-532-50
; Sequence 50, Application US/08479532
; Patent No. 5776752

GENERAL INFORMATION:

; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; TITLE OF INVENTION: Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,532
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/297,494
; FILING DATE: 08/297,494
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5776752and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2693 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 176..2077
; US-08-479-532-50

Query Match 19.3%; Score 598; DB 1; Length 2693;

Best Local Similarity 67.9%; Pred. No. 2,4e-154;
Matches 851; Conservative 0; Mismatches 400; Indels 3; Gaps 1;

QY 173 AGGCTGCCCTACATGGTGAAGCAGTTGGAGATGGGAGATAAACATTTGAGGAGCTGAAG 232
Db 302 AGATTACGGTCTTTGGTCAACAAATTAGAGAGAGGGGAGCTTCAGTGTGTAGATCTTAAG 361
QY 233 AAAAATCTGGAGTACACAGCTTCTGCTGGAAGCCGCTACATAGATGAGACACGGCAA 292
Db 362 AAGAATTTGGAATATGCAGCCACAGCTGCTGTAATCTGTATATTGATGAAACAGGAGA 421
QY 293 ATCTTGGACACCGGAGCAGCTGCGGTGAGAGCTGCGGTGAGATGCGGTGCTTCGAGGTG 352
Db 422 CTCCTGATACAGAGGATGAGCTCAGTGACATTCAGTGTGCTGCTTCTGAGGTC 481
QY 353 CGGGAGCTGGCTGCCCTCCACCTTACCCAGAGAGCCGGGCGGCAAGCCGCGGAGAGAG 412
Db 482 CGAGAGCTGGCTGCCCTCCACCTTACCGCGGAGATGGGGATGATGCTCAGAGAGAGCGAC 541
QY 413 GAGAAGCCCAAGTTCGAGAGCATTTGACAGCTGTGCGAGCTGGGATCTTCGTGGAGCG 472
Db 542 GAGAAGCCCGGTTCAAGAGCATGTTACCGAGTGCAGGCTGGGATATTGTTGGAGAGA 601
QY 473 ATGTTCCGGAGAACATACACCTTCTGTGGGCGCCACTTACTCTACTCGGTTCTCAACTGT 532
Db 602 ATGTATAGAGGACATCAACATGGTTGGACTGAGCTATCCACCAGCTGTTATTGAGGCA 661
QY 533 CTCAGAAGCTCGATCTCTGCTGCTTGTATGCTTTTCTTCTTGAACAGCAGCAGATGAC 592
Db 662 TTAAGAGATGTGCAAGTGGTCTTTGACGCTTTTCCCTCAATGAGGCCAGTGGGAT 721
QY 593 CATGCCCTGAGGACCATTTGTTTGTAGTTGCTGAGCTGCGCATACCTCATCAGCCCTTC 652
Db 722 CATGCATGAAATTTATTTTCTATGAACCTACTCACACGTTATGATCTGATCAGCCGTTTC 781
QY 653 AAGATTCACCTGTGTTTGTGATGAGTTTCTTCCGTGCTTGGAGAGCTGATGGAAG 712
Db 782 AAGATTCACCTTCTGCACTTCTCTCATTTTGGAGGCCCTGGAAGTGGGATACAGCAAG 841
QY 713 TACAAGAAATCTTACCAACACAGATCCACGAGCGGATGTTTACCCAGAGAGTCCATTCG 772
Db 842 CACAAAATCTTACCATTAATGACAGCTGCGGATGTTTACACAGACAGTGCATTAC 901
QY 773 TTTCTGCTCCGACAGGAGTGGTGCATGCTGCTGCGGAGATTGAGCTCTCTGGCCATCATC 832
Db 902 CTCCTCTATAAGACAGGAGTGGCGAAGCTGGCTACGGAGCTGGAGATCTTTGCTATAATC 961

Db 962 TTCTCAGCTGCCATCCATCACTAGAGCATACCGGAACCAACAAATTTCCACATTCAG 1021
QY 893 ACCAAGTCAGATGCGCATCGTGTACAAATGATCCTTCAGTCTCGAGAATCACCACATC 952
Db 1022 ACTCGGTGTATCCAGCTATTCTGTATATACAGATCTGTACTGGAGAATCACCATTTA 1081
QY 953 AGCTCTGTTTCCGATGATGAGGATGATGAG---ATGAACATTTTTCATCAACCTCACC 1009
Db 1082 AGTCAGCTTATCGCTTCTGCAAGATGACGAGGAATGAATATTTGATTAACCTCTCA 1141
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RESULT 15

US-08-455-525-50

Sequence 50, Application US/08455525

Patent No. 5800987

GENERAL INFORMATION:

APPLICANT: Beavo, Joseph A.

APPLICANT: Bentley, Kelley

APPLICANT: Charbonneau, Harry

APPLICANT: Sonnenburg, William K.

TITLE OF INVENTION: DNA Encoding Mammalian

TITLE OF INVENTION: Phosphodiesterases

NUMBER OF SEQUENCES: 58

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

ADDRESSEE: Bicknell

STREET: Two First National Plaza, 20 South Clark

STREET: Street

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60603

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/455,525

FILING DATE: 31-MAY-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/297,494

FILING DATE:

APPLICATION NUMBER: US 07/688,356

FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5800987 and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30822
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 2693 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
NAME/KEY: CDS
LOCATION: 176..2077
US-08-455-525-50

Query Match 19.3%; Score 598; DB 1; Length 2693;
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Matches 851; Conservative 0; Mismatches 400; Indels 3; Gaps 1;

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1347.6	43.6	1844	10	US-09-883-825-26	Sequence 26, Appl
2	668	21.6	722	13	US-10-027-832-21270	Sequence 21270, A
3	598	19.3	2693	10	US-09-883-825-50	Sequence 50, Appl
4	579.8	18.8	2656	10	US-09-883-825-16	Sequence 16, Appl
5	578.8	18.7	1625	10	US-09-883-825-48	Sequence 48, Appl
6	559.6	18.1	2291	10	US-09-883-825-5	Sequence 5, Appl
7	449.6	14.5	2077	10	US-09-883-825-52	Sequence 52, Appl
8	348	11.3	412	10	US-09-883-825-22	Sequence 22, Appl
9	221.4	7.2	467	11	US-09-918-995-10535	Sequence 10535, A
10	169.2	5.5	3890	9	US-09-947-305-1	Sequence 1, Appl
11	165.2	5.3	3705	10	US-09-880-107-2175	Sequence 2175, Ap
12	165.2	5.3	3705	10	US-09-954-531-1023	Sequence 1023, Ap
13	104.8	3.4	445	11	US-09-918-995-12257	Sequence 22257, A
14	101.8	3.3	470	9	US-09-864-761-11178	Sequence 11178, A
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16	93.8	3.0	1723	11	US-09-989-442-22	Sequence 22, Appl

17	86.4	2.8	3165	11	US-09-966-781A-11	Sequence 11, Appl
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20	85.4	2.8	1887	14	US-10-083-620A-18	Sequence 18, Appl
21	85.4	2.8	1967	14	US-10-083-620A-20	Sequence 20, Appl
22	85.4	2.8	1997	9	US-09-802-741A-2	Sequence 2, Appl
23	84.6	2.7	1457	14	US-10-083-620A-22	Sequence 22, Appl
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34	68.8	2.2	3789	10	US-09-883-825-42	Sequence 42, Appl
35	68.8	2.2	4131	10	US-09-883-825-38	Sequence 38, Appl
36	66.4	2.1	915	9	US-09-764-898-136	Sequence 136, App
37	66.4	2.1	915	11	US-09-989-442-48	Sequence 48, Appl
38	63	2.0	3221	9	US-09-815-825-19	Sequence 19, Appl
39	60.2	1.9	470	11	US-09-918-995-23930	Sequence 23930, A
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43	54.2	1.8	3231	14	US-10-175-523-149	Sequence 149, App
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ALIGNMENTS

RESULT 1

US-09-883-825-26
; Sequence 26, Application US/09883825
; Patent No. US20020151024A1
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; Bentley, Kelley
; Charbonneau, Harry
; Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; Phosphodiesterases
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; Bicknell
; STREET: Two First National Plaza, 20 South Clark
; Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/883,825
; FILING DATE: 18-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/123,783
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/297,494
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20020151024A1and, Greta E.

REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30822
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 1844 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 114..1715
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-883-825-26

Query Match 43.5%; Score 1347.6; DB 10; Length 1844;
Best Local Similarity 90.5%; Pred. No. 0;
Matches 1473; Conservative 0; Mismatches 144; Indels 9; Gaps 3;

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Sequence 21270, Application us/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
POLYMORPHISMS IN THE HUMAN GENOME
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30

Query Match	21.6%	Score 668;	DB 13;	Length 722;
Best Local Similarity	98.8%	Pred. No. 8.8e-193;		
Matches 681; Conservative 1;	Mismatches 6;	Indels 1;	Gaps 1;	

QY	1888	GGGAACATTACAGGCTCCACAGTGGTCACTGTGCCCATCCCTCAGACTCTCGGATTCCTTCAT	1947
DB	690	GGGACATTACAGGCTCCACAGTGGTCACTGTGCCCATCCCTCAGACTCTCGGATTCCTTCAT	632
QY	1948	GGCCAGGTGCTGCCAGGAGCGGGAGCTTCCTGGAGGCTTCCAGGGCTTGGGGAAG	2007
DB	631	GGCCAGGTGCTGCCAGGAGCGGGAGCTTCCTGGAGGCTTCCAGGGCTTGGGGAAG	572
QY	2008	GGTCAGAGATGCCAGGCCCTCGGACCTCCCCATCCTTTTGGCTCCAAAGTTCTAAGC	2067
DB	571	GGTCAGAGATGCCAGGCCCTCGGACCTCCCCATCCTTTTGGCTCCAAAGTTCTAAGC	512
QY	2068	AATACATTTTGGGGTTCCCTCAGCCCCCACCACCCAGATCTTAGCTGGCAGGCTCGGGTG	2127
DB	511	AATACATTTTGGGGTTCCCTCAGCCCCCACCACCCAGATCTTAGCTGGCAGGCTCGGGTG	452
QY	2128	CCCTCTTTTCCCTCCCTGGGAAGGCTGGAAATAGGATAGAAAGCTGGGGTTTTCAGAGCC	2187
DB	451	CCCTCTTTTCCCTCCCTGGGAAGGCTGGAAATAGGATAGAAAGCTGGGGTTTTCAGAGCC	392
QY	2188	CTATGTGTGGGAGGGAGTGGATTCTTCAGGGCATGGTACCTTTCTAGAGTCTGGGAA	2247
DB	391	CTATGTGTGGGAGGGAGTGGATTCTTCAGGGCATGGTACCTTTCTAGAGTCTGGGAA	332
QY	2248	TGGGTTGGAGAGACATCCTTTCACCCAGAAATGGGCTGCTTCAGCCCCCATCTCCAGC	2307
DB	331	TGGGTTGGAGAGACATCCTTTCACCCAGAAATGGGCTGCTTCAGCCCCCATCTCCAGC	272
QY	2308	CTGATCCTCTGAATCTTCTTCCCTCCTTCTCTGATACAGTGACTGGGGCAAAAGAGACC	2367
DB	271	CTGATCCTCTGAATCTTCTTCCCTCCTTCTCTGATACAGTGACTGGGGCAAAAGAGACC	212
QY	2368	ATTGTGACAGGGCTGCGGAGGCCCTTCTCGGGACCTTCTTTGGGACTGGTCTGGGCC	2427
DB	211	ATTGTGACAGGGCTGCGGAGGCCCTTCTCGGGACCTTCTTTGGGACTGGTCTGGGCC	152
QY	2428	CTTGGGCTGTGCGCTGCCCTGAGTCCGAGGCCCTTGGCTCCTTCTCTCCCTCGGGG	2487
DB	151	CTTGGGCTGTGCGCTGCCCTGAGTCCGAGGCCCTTGGCTCCTTCTCTCCCTCGGGG	92
QY	2488	CTGGGAGCTCCATCCGACCAATGCTGTAAGTGTCTTGAGGATCTCCCCAGCAAGACA	2547
DB	91	CTGGGAGCTCCATCCGACCAATGCTGTAAGTGTCTTGAGGATCTCCCCAGCAAGACA	32
QY	2548	CCTTCAGATGTATCGACACACAGCTGGT	2576
DB	31	CCTTCAGATGTATCGACACACAGGGGAT	3

us-09-663-481-2.rnpb

Mon Aug 11 15:23:54 2003

1502 ACAGCATGACCGAGAGATTTGTGATCCATTATTCGATGAACCTCTCAAACT 1555

Db	422	CTCCTGGATACAGAGATGAGCTCAGTACATTCAGTCAGATGCTGTGCTCTTCTGAGTC	481
QY	353	CGGACTGCTGGCTCCACCTTCACCCAGCAGGCGCGGCAAGGCGCGCCGAGCAG	412
Db	482	CGAGACTGCTGGCTCCACCTTCACCCAGCAGGCGCGGCAAGGCGCGCCGAGCAG	541
QY	413	GAGAAGCCCAAGTTCCGAAGCATTTGTGCAGCTGTGCAGGCTGGATCTTCTGGAAGG	472
Db	542	GAGAAGCCCGGTTCAAGAGCATCGTTTCAGCAGGTCAGGCTGGATTTTGGGAGA	601
QY	473	ATGTTCCGGAGAGATACACCTCTGTGGGCCCCACTTACTACTACGCTTCTCACTGT	532
Db	602	ATGATAGACGGACATCAACATGTTGGAGTGTGAGCTATCCACGCTGTATTGAGCA	661
QY	533	CTCAAGAACCTGGATCTGGTCTTGTGATGCTTTTCTTGTGACCCAGCAGCATGAC	592
Db	662	TAAAGGATGTGGACAGTGTCTTTGAGCTTTTCCCTCANTAGGCCGCTGCGGAT	721
QY	593	CATGCTGAGGACCATTTGTTGATGCTGCTGACTCGGCAATCACTCATCAGCGCTTC	652
Db	722	CATGACTGAAATTTATTTCTATGAATCTACTCAGCTTTATGATCTGATCAGCGCTT	781
QY	653	AAGATCCCACTGTTTGTGATGAGTTTCTGATGCTTCTGATGCTTGTGAGCAGCTAT	712
Db	782	AAGATCCCACTGTTTGTGATGAGTTTCTGATGCTTCTGATGCTTGTGAGCAGCTAT	841
QY	713	TACAGAACTCTTACCAACAGATCCAGCAGGCGCATGTATACCCAGCAGTCCATTGC	772
Db	842	CACAAAATCTTACCAACAGATCCAGCAGGCGCATGTATACCCAGCAGTCCATTGC	901
QY	773	TCTTGTGCTCGGACAGGATGTTGATGAGTTTCTGATGCTTCTGATGCTTGTGAGC	832
Db	902	CTTCTCTTATAGCAGGAGTGGCAACTGCTGAGGAGCTGGAGATCTTTGCTATATC	961
QY	833	TTTGTGCTGATCATCATGATATGACGACAGGCGCATGTATACCCAGCAGTCCATTGC	892
Db	962	TTTGTGCTGATCATCATGATATGACGACAGGCGCATGTATACCCAGCAGTCCATTGC	1021
QY	893	ACCAATGAGATGTGCCATCTGTACATGATCTGTGAGTGTGAGCTGCTGGCCATCATC	952
Db	1022	ATCTGCTGATCCAGCTATCTGTATATGATGATGATGAGTGTGAGCTGCTGGCCATCATC	1081
QY	953	AGCTCTGTTTCCGATGATGAGGATGATGAGTGTGAGCTGCTGGCCATCATC	1009
Db	1082	AGTGCAGCTATCCGCTTCTGCAAGATGACGAGGAATGAATTTTGAATTAACCTCTCA	1141
QY	1010	AAGATGAGTTTCTGAGAACTCCGAGCCTGCTGATGATGATGATGATGATGATGATG	1069
Db	1142	AAGATGAGTTTCTGAGAACTCCGAGCCTGCTGATGATGATGATGATGATGATGATG	1201
QY	1070	TCTGCTGATTTCCAGCAAGTGAAGACCATGAAGACAGCTTGAACAGCTGGAGGAT	1129
Db	1202	TCTTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1261
QY	1130	GACAAGCCCAAGGCTTCTCTACTGCTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCT	1189
Db	1262	GAAAAGCCCAAGGCTTCTCTACTGCTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCT	1321
QY	1190	CAGTGTGTTGCTCCAGCCGTTGACCAAGCCCTCATGAGAGATTTCTTCCCTCAGGT	1249
Db	1322	GCATGGGACCTCCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1381
QY	1250	GACAAGGAGGAGAGTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1309
Db	1382	GACAGAGAGGAGAGTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1441
QY	1310	GTGGCAGATCTCAGATAGGTTTCAATGATGATGATGATGATGATGATGATGATGATG	1369
Db	1442	GTGTGCTGATCAAGTAGGTTTCAATGATGATGATGATGATGATGATGATGATGATG	1501
QY	1370	ACTGAGCTGGCAGAGAGTGTTCAGCCCTGCGGATGAGGACTCCAACTCT	1423

RESULT 4
 US-09-883-825-16
 ; Sequence 16, Application US/09883825
 ; Patent No. US20020151024A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Beavo, Joseph A.
 ; Bentley, Kelley
 ; Charbonneau, Harry
 ; Sonnenburg, William K.
 ; TITLE OF INVENTION: DNA encoding Mammalian
 ; Phosphodiesterases
 ; NUMBER OF SEQUENCES: 58
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 ; STREET: Two First National Plaza, 20 South Clark
 ; Street
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60603
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/883,825
 ; FILING DATE: 18-Jun-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 09/123,783
 ; FILING DATE: <Unknown>
 ; APPLICATION NUMBER: 08/297,494
 ; FILING DATE: <Unknown>
 ; APPLICATION NUMBER: US 07/688,356
 ; FILING DATE: 04-APR-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: No. US20020151024Aland, Greta E.
 ; REGISTRATION NUMBER: 35,302
 ; REFERENCE/DOCKET NUMBER: 27866/30822
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (312) 346-5750
 ; TELEFAX: (312) 984-9740
 ; TELEX: 25-3856
 ; INFORMATION FOR SEQ ID NO: 16:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2656 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 136..1677
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
 US-09-883-825-16
 Query Match 18.8%; Score 579.8; DB 10; Length 2656;
 Best Local Similarity 64.8%; Pred No. 1.3e-165;
 Matches 883; Conservative 0; Mismatches 472; Indels 0; Gaps 0;
 QY 101 AGCAGGAACCTTGTATCCCATGCGCAACCTGTTCTGTTTCAGAGGAGCCACCTCCAG 160
 Db 115 AGCTTAATCTTCCACCTTTAAATGGATGACCATGTCCAAATCAGGAGGAAACATCTCCAA 174
 QY 161 GGCCCATCTTCAGCTGCGCTACATGGTGAACCACTTGGAGATGGGAGATTAACATT 220
 Db 175 AGACCATCTTTAGACTAAGATGCTTAGTGAAGCAGCTGGAAGAAAGGTGATGTTAAGCTC 234

QY 221 GAGGAGCTGAAGAAAAAATCTGGAGTACACAGCTCTCTGCTGGAAGCCGCTACATAGAT 280
DB 235 ATCGACTTAAAGAGAATATTGAATATGACAGTCTGTGTTGGAAGCAGTTTATATTGAT 294
QY 281 GAGACACGGCAAAATCTTGGACACGAGGACAGCTGCGAGCTGCGGTGAGATCCGCTG 340
DB 295 GAACACAGGAGACTGCTGGACACGAGTATGAGCTCAGTGACATTCAGTCGGATTCGCTG 354
QY 341 CTTTCGGAGTGCAGGAGTCTGCTGCTCCACCTTCCACCCAGCAGCGCCGCGCAAGGC 400
DB 355 CCATCAGAAGTCCGGAGCTGTTGCTTCTACCTTTACACGGAATGGGATGATGAA 414
QY 401 CGCCGACAGAGGAGAGCCCAAGTTCGGAAGCATTTGTCACGCTGTCAGCGCTGGGATC 460
DB 415 AAGAAATCTGAGAAAAACCAAGATTTCCGAGCATTTGTCATGTTTCAAGCTGGAAT 474
QY 461 TTCGTGGAACGATGTTCCGAGAACATACACCTCTCTGGGCCCCACTTACTCTACTGCG 520
DB 475 TTTGTGGAAGATGTACAGAAAGTCTTATCAGATGTTGCTGGCATATCCAGAGGCT 534
QY 521 GTTCTCAACTGCTCAAGAACTGATCTCTGCTGCTTTGATGCTTTTCTTGAACCCAG 580
DB 535 GTCATAGTAACTTAAGAGTGTGATAAATGGTCTTTGATGATTTGCTTGAATGAA 594
QY 581 GCAGAGATGACCATGCGCTGAGGACCATGTTTGTGATGCTGCTGCTGCTGCTGCTG 640
DB 595 GCAAGTGGAGAACACAGCTGCTGAAGTTTATGATTTATGAACCTATTCACGAGATGATCTT 654
QY 641 ATCAGCCGCTTCAAGATTCACACCTGCTGTTTGTGATGATGCTTCTGCTGCTGAGACA 700
DB 655 ATCAACCGTTTCAAGATTCCTGCTTCTTTCCTTAATGCTTGTGAGAGAGCTCTAGAAGTT 714
QY 701 GGCTATGGGAAGTACAAGAACTCTTACCACAAACAGATCCACGCGCGATGTTACCCAG 760
DB 715 GGTACAGCAAGTACAAAATCCATACCAATTTGATTCATGACGCTGATGCTACTCAA 774
QY 761 ACAGTCCATGCTCTGCTGCTCGGACAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 820
DB 775 ACTGCTATACAAATGCTCTATACAGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 834
QY 821 CTGCGCATCATCTTTGCTGAGCTATCATGATGAGCAGCAGCGGCGCTTACCAACAGC 880
DB 835 TTGACATGCTTTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 894
QY 881 TTCACATCCACCAAGTCAAGATGTGCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 940
DB 895 TTTACATTCAGACAAAGTCAAGTGTGCCATTTGATATGATGCTGCTGCTGCTGCTGCTG 954
QY 941 AATCACCATCAGCTCTGTTTCCGATGATGAGGAGTATGATGATGATGATGATGATGATG 1000
DB 955 AATCATCATGTGAGTGCAGCTTATCGCCTTATGCAAGAAAGAAATGAATGCTGCTGATA 1014
QY 1001 AACCTCACCAAGGATGATTTGTAGAACTCCGAGCCCTGCTGCTGCTGCTGCTGCTGCTG 1060
DB 1015 AATTATTCGAAGATGACTGGAGGATCTTCGGAACCTAGTGTGATGATGATGATGATGATG 1074
QY 1061 ACAGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1120
DB 1075 ACAGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1134
QY 1121 GAGAGGATGACAAAGCCCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1180
DB 1135 GAAGGGCTTGACAAAGCCCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1194
QY 1181 CCAACCAAGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1240
DB 1195 CCAGCCAAATCTGGAAGCTGACACCGATGGACCATGGCCCTTAATGGAGGATTTTC 1254
QY 1241 CGTCAGGCTGACAAAGGAGGAGTGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1300
DB 1255 CTACAGGAGATGAAGAGCTGAATAGGGCTTCCATTTCCCGCTTGGGATCGGAG 1314
QY 1301 TCCACTAGTGGCAGAGTCTCAGATAGAGGTTTCAGACTTTCATTTGTTGGAGCCCACTTC 1360

DB 1315 TCAACGATGTTGGCCAGTCCCAATAGTTTCATTTGATTTTCATAGTAGAACCAACATTT 1374
QY 1361 TCTGTGCTGACTGAGTGGCAGAGAGAGTCTTCAGCCCTGCGGATGAGGACTCCCAAG 1420
DB 1375 TCTCTCTGACAGACTCAACAGAGAAATTTATTTCTCTTATAGAGGAAGACTCGAAA 1434
QY 1421 TCTAAAAACCCAGCCC 1435
DB 1435 ACCAAAACCTCTCC 1449

RESULT 5

US-09-883-825-48
; Sequence 48, Application US/09883825
; Patent No. US20020151024A1
GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; Bentley, Kelley
; Charbonneau, Harry
; Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; Phosphodiesterases
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; Bicknell
; STREET: Two First National Plaza, 20 South Clark
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/883,825
; FILING DATE: 18-Jun-2001
; CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/123,783
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/297,494
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
; NAME: No. US20020151024Aland, Greta E.
; REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30822
TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
; LENGTH: 1625 base pairs
; TYPE: nucleic acid
STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
FEATURE:
; NAME/KEY: CDS
; LOCATION: 12..1616
SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-09-883-825-48

Query Match 18.7%; Score 578.8; DB 10; Length 1625;
Best Local Similarity 66.0%; Pred. NO. 2e-165;
Matches 838; Conservative 0; Mismatches 432; Indels 0; Gaps 0;

US-09-883-825-5

Query Match	18.1%	Score	559.6	DB	10	Length	2291
Best Local Similarity	64.9%	Pred. No.	1.7e-159				
Matches	829	Conservative	0	Mismatches	449	Indels	0
QY	158	CAGGGCCCCATTCTCAGGCTCGCCTACATGCTGAAGCAGTTGGAGAAATGGGAGATAAAC	217				
DB	184	CAACGCTGAAGGAATACTAAGATGCTTAGTGAAGCAGCTGGAANAAGGTGATGTTAAC	243				
QY	218	ATTGAGAGCTGAAGAAAATCTGGAGTACACAGCTTCTGCTGGAAGCGCTCATATA	277				
DB	244	GTCAATGCATTAAGAAGAAATATGAATATGCAGCATCTGTGTGGAAGCAGTTTATATT	303				
QY	278	GATGAGACGCGCAAAATCTTGGACACGGAGACGAGCTGCAGGAGCTGCGGTCCAGATGCC	337				
DB	304	GATGAACACAGGAGACTGCTGGACACCGATGATGAGCTAGTGCATTCAGTCGGATGCC	363				
QY	338	GTGCTTCGGAGTGGGGACTGGCTGGGCTCCACCTTCACCCAGCAGGCCCGGGCCAAA	397				
DB	364	GTCCCATCAGAAGTCGGGACTGGTTGGCTTCTACCTTTACAGGAAAATGGGGATGATG	423				
QY	398	GGCGCGGACGAGAGAGACCCCAAGTTCGGAAGCAATGTGACAGCTGTGCAGGCTGGG	457				
DB	424	AAAAGAAATCTCAGGAAAACCAAGATTTCCGGAGCATGTGCGATGTGTTCAAGCTGGA	483				
QY	458	ATCTTCGTGGAACGGATGTTCCGGAGAACATACACCTCTGTGGGCCCCACTTACTCTACT	517				
DB	484	ATTTTTGTGAAAGATGTACAGAAAGTCCTATCACATGGTTGCTGGCATATCCAGAG	543				
QY	518	CGCGTCTCAACTGCTCAAGAACCTGGATCTCTGGTGCTTTGATGCTTTTCCCTGGAAC	577				
DB	544	CGTGTCTATAGTAACATTAAGAGATGTGATAAATGGTCTTTTGTATGTTATTTGGCTTGAAT	603				
QY	578	CAGCGACGACATGACCATGCCCTGAGGACCAATGTTTTGAGTTGCTGACTCGGCATAAC	637				
DB	604	GAAGCAAGTGGAGACACAGCTGGAAGTTTATGATTTATGAACTATTCACCATATGAT	663				
QY	638	CTCATCAGCGCTTCAAGATPCCCATCTGTTTTGATGAGTTTCTCTGGATGCTTTGGAG	697				
DB	664	CTTATCAACGGTTTCAAGATTCCTGTTCTTGCTTAATTGCCCTTTCGAGAAGCTCAGAA	723				
QY	698	ACAGGCTATCGGAAGTACAGAAATCCTTACCACACAGATCCACGACGCGGATGTACC	757				
DB	724	GTGTGTTACAGCAAGTACAAAATCCATACCAAAATTTGATTCAGCGTGATGTCAT	783				
QY	758	CAGACAGTCCATGCTTCTTGCTCCGACAGGATGGTGACCTGCTCGGAGATTGAG	817				
DB	784	CAAACTGTGCATTACATAATGCTTCTACAGGTATCATGCACCTGGCTCACTGAACGGAA	843				
QY	818	CTCCTGGCCATCATCTTTGCTGCACTATCCATGATATGAGCACACGGGCATACCAAC	877				
DB	844	ATTTTAGCAATGGTCTTTGGCGTGGCCATTCATGACTATGAGCATACAGGGACTACAAAC	903				
QY	878	AGCTTCCACATCAGACCAAGTCAGATGCGCATGCTGTACATGATCCTTCAGTGCCTG	937				
DB	904	AAITTTTCATCTCAGACAGGTGAGATGTTGGCCATTTTGTATGATGATCCTCTGTCCTT	963				
QY	938	GAGAATCACCACATCAGCTCTGTTTTCCGATTGATGCAAGGATGATGAGATGAACATTTTC	997				
DB	964	GAAAATCATCATGTGAGTGCAGCTTATCGCCTTATGCAAGAAGAANAATGAATGTCCTG	1023				
QY	998	ATCAACCTCACCAGGATGATTTGTAGAACTCCGAGCCCTGGTCAATGAGATGGTGGTTG	1057				
DB	1024	ATAAATTTATCCAAAGATGACTGGAGGGATCTTTCCGNAACCTAGTGTGAATGGTGGTG	1083				
QY	1058	GCCACAGACATGCTCTGCCATTTCCAGCAAGTGAAGACCATTGAAGACAGGCTTTGCAACAG	1117				
DB	1084	TCFACAGACATGTCGGGTCACTCCAGCAAAATTAANAATATAGAAATAGTTTGCAGCAA	1143				
QY	1118	CTGAGAGGATTGACAAGCCCAAGGCCCTGCTCTACTGCTCCATGCTGTCATCAGC	1177				
DB	1144	CCTGAAGGGCTTGACAAAGCCCAAAACCATCTCCCTGATCTCCATCAGCAGACATCAGT	1203				

RESULT 7

US-09-883-825-52
: Sequence 52, Application US/09883825
: Patent No. US20020151024A1
: GENERAL INFORMATION:
: APPLICANT: Beavo, Joseph A.
: Bentley, Kelley
: Charbonneau, Harry
: Sonnenburg, William K.
: TITLE OF INVENTION: DNA Encoding Mammalian
: Phosphodiesterases
: NUMBER OF SEQUENCES: 58
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
: Bicknell
: STREET: Two First National Plaza, 20 South Clark
: Street
: CITY: Chicago
: STATE: Illinois
: COUNTRY: USA
: ZIP: 60603
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/883,825
: FILING DATE: 18-Jun-2001
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 09/123,783
: FILING DATE: <Unknown>
: APPLICATION NUMBER: 08/297,494
: FILING DATE: <Unknown>
: APPLICATION NUMBER: US 07/688,356
: FILING DATE: 04-APR-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: No. US20020151024Aland, Greta E.
: REGISTRATION NUMBER: 35,302
: REFERENCE/DOCKET NUMBER: 27866/30822
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (312) 346-5750
: TELEFAX: (312) 984-9740
: TELEX: 25-3856
: INFORMATION FOR SEQ ID NO: 52:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2077 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear

DB	903	CGGAGAGATTGTGAGTCCATTAATCATGAACAACTTCAACT	946
RESULT 8			
US-09-883-825-12			
Sequence 22, Application US/09883825			
Patent No. US/20020151024A1			
GENERAL INFORMATION:			
APPLICANT: Beavo, Joseph A.			
Bentley, Kelley			
Charbonneau, Harry			
Sonnenburg, William K.			
TITLE OF INVENTION: DNA Encoding Mammalian			
Phosphodiesterases			
NUMBER OF SEQUENCES: 58			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &			
Bicknell			
STREET: Two First National Plaza, 20 South Clark			
Street			
CITY: Chicago			
STATE: Illinois			
COUNTRY: USA			
ZIP: 60603			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Floppy disk			
COMPUTER: IBM PC compatible			
OPERATING SYSTEM: PC-DOS/MS-DOS			
SOFTWARE: Patentin Release #1.0, Version #1.25			
CURRENT APPLICATION DATA: US/09/883,825			
FILING DATE: 18-Jun-2001			
CLASSIFICATION: <unknown>			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: 09/123,783			
FILING DATE: <unknown>			
APPLICATION NUMBER: 08/297,494			
FILING DATE: <unknown>			
APPLICATION NUMBER: 07/688,356			
FILING DATE: 04-Apr-1991			
ATTORNEY/AGENT INFORMATION:			
NAME: No. US20020151024Aland, Greta E.			
REGISTRATION NUMBER: 35,302			
REFERENCE/DOCUMENT NUMBER: 27866/30822			
TELEPHONE: 312 346-5750			
TELEFAX: 312 984-9740			
INFORMATION FOR SEQ ID NO: 22:			
SEQUENCE CHARACTERISTICS:			
LENGTH: 412 base pairs			
TYPE: double-stranded			
STRANDNESS: single			
TOPOLOGY: linear			
MOLECULE TYPE: cDNA			
FEATURE:			
NAME/KEY: CDS			
LOCATION: 1..412			
SEQUENCE DESCRIPTION: SEQ ID NO: 22:			
US-09-883-825-22			
Query Match 11.3%; Score 348; DB 10; Length 412;			
Best Local Similarity 90.3%; Pred. No. 2.3e+95;			
Matches 372; Conservative 40; Indels 0; Gaps 0;			
QY	845	ATCCATGATTATGACACACGGGCACCTACCAACAGCTTCACATCCACAGAACAGTGAGAA	904
Db	3	ATTCATGATTATAACACACGGGCACCTACCAACAGCTTCACATCCACAGAACAGTGAGAA	60
QY	905	TGTGCCATGCTACAATGCTTCACTGCTGGAGATACCACATCAGCTCTGTTC	964
Db	61	TGCGCATCTCTGTACAACAGCGCTCAGTCTGGAGATACCACATCAGCTCTGTTC	120

QY 965 CGATTGTCAGGATGATGAGATGAACATTTTCATCAACCTCACCAGGATGAGTTGTA 1024
Db 121 CGAATGTCAGGACGACATGAACATCTTCATCAACCTCACCAGGATGAGTTGTA 180
QY 1025 GAATCCGAGCCCTGGTCATTGAGATGGTGTGGCCACAGACATGCTGCCATTTCCAG 1084
Db 181 GAGCTGGGGCTCTGGTCATTGAGATGGTGTGGCCACAGACATGCTGCCATTTCCAG 240
QY 1085 CAAGTGAAGACCATGAAGACAGCCTTGCAACAGCTGGAGAGATTGCAAGCCCAAGGCC 1144
Db 241 CAAGTGAAGTCATGAAGACAGCCTTGCAAGCTGGAGAGATTGCAAGTCCAAGGCC 300
QY 1145 CTGTCTCTACGTCTCCATGCTGTCGATCATCAGCACCACCAACCAAGCAGTGGTGGTCCAC 1204
Db 301 CTCTCTCTGCTCTTCATGCTGCTGATCATCAGCACCACCAACCAAGCAGTGGTGGTCCAC 360
QY 1205 AGCGGTGGACCAAGGCCCTCATGGAGGAATCTTCGTCAAGGTGACAAAG 1256
Db 361 AGCGGTGGACCAAGGCCCTCATGGAGGAATCTTCGTCAAGGTGACAAAG 412

RESULT 9
US-09-918-995-10535
; Sequence 10535, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10535
; LENGTH: 467
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(467)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-10535

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Best Local Similarity 70.2%; Pred. No. 9.5e-57;
Matches 297; Conservative 0; Mismatches 126; Indels 0; Gaps 0;

QY 852 ATTATGACACACGGGCACTACCAACAGCTTCCACATCCACAGCAAGTCAGAAATGTGCCA 911
Db 44 ATTCTGACATACAGGACAAACAACACTTTCATTCACATTCACAGAGGTCAGATGTGCCA 103
QY 912 TCGTGTACAATGATCGTTTCAGTGTGGAGAAATCACCACATCAGCTCTGTTTCCGATGA 971
Db 104 TTTTGTATATGATCGCTCTGCTGCTGAGATCACCAGTCCAGTGCACCTATCGACTTA 163
QY 972 TGCAGGATGATGAGATGACATTTTCATCAACCTCACCAGGATGAGTTGTAGAACTCC 1031
Db 164 TCGAAGAAGAAGAATGAATATCTTGATAAATTTTCAAAAGATGACTGGAGGATCTTC 223
QY 1032 GAGCCCTGGTCATTGAGATGGTGTGGCCACAGACATGCTCTGCCATTTCCAGCAAGTGA 1091
Db 224 GGAACCTAGTATGAAATGGTTTATCTACAGACATGTTCAGGTCACCTCCAGCAAAATTA 283
QY 1092 AGACCTGAAGACAGCCTTGAACAGCTGGAGAGATTGCAAGCCCAAGGCCCTGTCTC 1151
Db 284 AAATATTAAGAAACAGTTTGCAGCAGCCTGAGGGATTGACAGCCCAAAACCATGTGCC 343
QY 1152 TACTGCTCCATGCTGATCATCAGCACCACCAAGCAGTGGTGGTCCACAGCCGTT 1211
Db 344 TGATTCTCCAGCAGCAGACATCAGCCACCACCCAGCCAAATCTCGAAGCTGCATTATCGGT 403

QY 1212 GGACCAAGGCCCTCATGTGAGGAATTTCTCCGTGAGGGTGACAAGGACGACAGATTGGGCC 1271
Db 404 GGACCATGGCCCTAATGAGGAGTTTTTCTCCAGGGAGATAAAGAACTGAATTAGGCC 463
QY 1272 TGC 1274
Db 464 TTC 466

RESULT 10
US-09-947-305-1
; Sequence 1, Application US/09947305
; Patent No. US20020068351A1
; GENERAL INFORMATION:
; APPLICANT: Livi, George P.
; APPLICANT: McLaughlin, Megan M.
; APPLICANT: Torphy, Theodore J.
; TITLE OF INVENTION: Human Brain Phosphodiesterase
; FILE REFERENCE: P50145C2D3
; CURRENT APPLICATION NUMBER: US/09/947,305
; CURRENT FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: 08/445,474
; PRIOR FILING DATE: 1995-05-22
; PRIOR APPLICATION NUMBER: PCT/US94/02612
; PRIOR FILING DATE: 1994-03-10
; PRIOR APPLICATION NUMBER: 08/029,334
; PRIOR FILING DATE: 1993-03-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3890
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-947-305-1

Query Match 5.5%; Score 169.2; DB 9; Length 3890;
Best Local Similarity 52.1%; Pred. No. 2.2e-40;
Matches 477; Conservative 0; Mismatches 403; Indels 36; Gaps 3;

QY 526 CAACTGTCTCAAGAACCTGGATCTCTGTGTCTTTGATGCTCTTTTCTTGAACCCAGGACG 585
Db 782 CAAGGAGCTGGAAGACCTGGAACAAATGGGGTCTTAACATCTTTAATGTGGCTGATATTC 841
QY 586 AGATCACCATGCCCTGAGGACCATGTTTTCAGTTGCTGACTCGGCATACCTCATCAG 645
Db 842 TCACAAATAGACCCCTAACATGATGATGCTATATTCAGGAAGAGACCTCCTAAA 901
QY 646 CCGCTTCAAGATTCCCACTGTGTTTGTGATGAGTTTCTCTGGATGCTTTGGAGACAGGCTA 705
Db 902 GACATTCAGATCTCATCTGACACATTTATAACCTACATGATGACTTTAGA---AGACCA 958
QY 706 TGGGAAGTACAGAAATCTCTTACCACACAGATCCACGAGCCGATGTTACCCAGACAGT 765
Db 959 TTACCATCTGACGTGGCATATCACACAGCCCTGCAACGCTGCTGATGATGAGCCAGTCGAC 1018
QY 766 CCATGTCTTCTGCTCCGACAGGATGTCACCTGCTGTCGGAGATGAGCTCTGCGC 825
Db 1019 CCATGTCTCTTCTTACACCCAGCATTAGACGCTGCTTTCACAGATTTGGAGATCCTGCG 1078
QY 826 CATCATCTTGTGTCAGCTATCCATGATTATGAGCACACGGGCACTACCAACAGCTTCCA 885
Db 1079 TGCCATTTTTCAGCTGCGCATCCATGAGTGTGATCATCTGAGGTCTCCAATCAGTTTCT 1138
QY 886 CATCCAGACCAAGTACAGATTCGTCATCGTGTACAAATGATCGTTCAGTGTGGAGAAATCA 945
Db 1139 CATCAACACAAATTCAGAACTTGTCTTGTATGTATAATGATGAATCTGTGTGGAAATCA 1198
QY 946 CCATCATCAGCTCTGTTTTCGATTCATGCAGGATGATGATGATGATGATGATGATGAT 1005
Db 1199 TCACCTTCTGTTGGTGTTCACAACTGCTGCAAGAAGAACACTGTGATCATCTTTCATGAT 1258
QY 1006 CACCAAGATGAGTTTGTAGAACTCCGAGCCCTGCTGATGATGATGATGATGATGATGAT 1065

Db	1259	CACCAAGAGGAGCGCTGACAGACTCAGAGAGATGGTTATTGACATGGTTAGCAACTGA	1318
Qy	1066	CATGCTGCCATTTCCAGCAAGTGAAGACCATGAAGA-----	1103
Db	1319	TATGCTAAACATATGAGGCTCTGGCAGACTGAGACAATGGTAGAACAAGAAAGT	1378
Qy	1104	-----CAGCCTTGCAACAGCTGGAGAGATTGACAGACCA---AGGCCCTGTCTCT	1152
Db	1379	TACAACTTCAGGGTTCCTCTAGACACACTATACCGATCCATTCAGGCTTCGCAAA	1438
Qy	1153	ACTGCTCCATGCTGACATGAGCAGCCACCCACAGCAGTGGTCCACAGCGGTG	1212
Db	1439	CATGGTACACTGTGACAGACTGACAAACCCACCAAGTCTCTTGAATTTATCGCAATG	1498
Qy	1213	GACCAAGGCCCTCATGAGGAATTTCCGTCAGGCTGACAAAGGAGGAGAGTTGGGCT	1272
Db	1499	GACAGCCGATCATGAGGAATTTTCCAGCAGGAGAGACAAAGAGCGGAGAGGGAAT	1558
Qy	1273	GCCTTTCTCCACTCTGTGACCGCACTTCCACTCTAGTGCGACAGCTCAGATAGGGT	1332
Db	1559	GGAAATTAGCCCAATGTGTAAACACACAGCTTCTGTGGAATAATCCAGGTTGGTT	1618
Qy	1333	CATCGACTTCATGTGAGCCCACTTCTCTGTGCTGACTGACGTGGCAGAGAGAGTGT	1392
Db	1619	CATCGACTACATGTCCATCCATTTGGGAGACATGGGAGATTTGGTACAGCCTGATG	1678
Qy	1393	TCAGCCCTGGCGGAT	1408
Db	1679	TCAGGACATTCGAT	1694
RESULT 11			
US-09-880-107-2175			
; Sequence 2175, Application US/09880107			
; Patent No. US20020142981A1			
; GENERAL INFORMATION:			
; APPLICANT: Horne, Darci T.			
; APPLICANT: Vockley, Joseph G.			
; APPLICANT: Scherf, Uwe			
; APPLICANT: Gene Logic, Inc.			
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer			
; FILE REFERENCE: 44921-5028-WO			
; CURRENT APPLICATION NUMBER: US 09/880,107			
; CURRENT FILING DATE: 2001-06-14			
; PRIOR APPLICATION NUMBER: US 60/211,379			
; PRIOR FILING DATE: 2000-06-14			
; PRIOR APPLICATION NUMBER: US 60/237,054			
; PRIOR FILING DATE: 2000-10-02			
; NUMBER OF SEQ ID NOS: 3950			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 2175			
; LENGTH: 3705			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 L20965			
US-09-880-107-2175			
Query Match 5.3%; Score 165.2; DB 10; Length 3705;			
Best Local Similarity 52.1%; Pred. No. 3.6e-39;			
Matches 445; Conservative 0; Mismatches 373; Indels 36; Gaps 2;			
Qy	533	CTCAAGAACTGGATCTGTGGCTTTGATGCTTTTCTTGAACAGCAGCAGATGAC	592
Db	1220	CTGGAGAACTGAACAAGTGGGCGCTTGTGCTGTGGATACCTGCGGATACCTGGAGC	1279
Qy	593	CATGCCCTGAGGACCAATGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	652
Db	1280	CGTCACTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1339
Qy	653	AGATGCCCACTGTGTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	712
RESULT 12			
US-09-954-531-1023			
; Sequence 1023, Application US/09954531			
; Patent No. US20020165180A1			
; GENERAL INFORMATION:			
; APPLICANT: Weaver, Zoe			
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using			
; FILE REFERENCE: 689290-77			
; CURRENT APPLICATION NUMBER: US/09/954,531			
; CURRENT FILING DATE: 2002-05-02			
; PRIOR APPLICATION NUMBER: US/60/233,133			
; PRIOR FILING DATE: 2000-09-18			
; PRIOR APPLICATION NUMBER: US/60/234,009			
; PRIOR FILING DATE: 2000-09-20			
; PRIOR APPLICATION NUMBER: US/60/234,034			
; PRIOR FILING DATE: 2000-09-20			
; PRIOR APPLICATION NUMBER: US/60/234,509			
; PRIOR FILING DATE: 2000-09-22			
; PRIOR APPLICATION NUMBER: US/60/234,567			
; PRIOR FILING DATE: 2000-09-22			
; NUMBER OF SEQ ID NOS: 1392			

Mon Aug 11 15:23:54 2003

us-09-663-481-2.rnpb

Page 13

Search completed: August 11, 2003, 01:06:30
Job time : 683 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 10, 2003, 17:33:05 ; Search time 5699 Seconds

(without alignments)
13182.161 Million cell updates/sec

Title: US-09-663-481-2

Perfect score: 3091

Sequence: 1 gtcgccaccgcgtccggga.....aaaaaaaaaaaaaaaaaaaaa 3091

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:**

2: em_esthum:**

3: em_estmu:**

4: em_estmu:**

5: em_estov:**

6: em_estpl:**

7: em_estro:**

8: em_estro:**

9: gb_estl:**

10: gb_est2:**

11: gb_estc:**

12: gb_est3:**

13: gb_est4:**

14: gb_est5:**

15: em_estfun:**

16: em_estom:**

17: em_gss_hum:**

18: em_gss_inv:**

19: em_gss_pln:**

20: em_gss_vrt:**

21: em_gss_fun:**

22: em_gss_mam:**

23: em_gss_mus:**

24: em_gss_pro:**

25: em_gss_rod:**

26: em_gss_phg:**

27: em_gss_vrl:**

28: gb_gss1:**

29: gb_gss2:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1612.4	52.2	2808	11 AK004772	AK004772 Mus muscu
2	734	23.7	786	12 B1488476	B1488476 603020977
3	665.2	21.5	878	10 BG390932	BG390932 602417604
4	643.4	20.8	749	13 BQ179638	BQ179638 UI-M-EVO-

5	636.8	20.6	737	13	BQ179626	BQ179626 UI-M-EVO-
6	600	19.4	2053	11	AK014887	AK014887 Mus muscu
7	600	19.4	2132	11	AK077123	AK077123 Mus muscu
8	599.6	19.4	2128	11	AK015375	AK015375 Mus muscu
9	599.6	19.4	3451	11	AK050499	AK050499 Mus muscu
10	599.6	19.4	3909	11	AK030423	AK030423 Mus muscu
11	599.6	19.4	4017	11	AK082180	AK082180 Mus muscu
12	599.6	19.4	4484	11	AK082497	AK082497 Mus muscu
13	599.6	19.4	4729	11	AK029531	AK029531 Mus muscu
14	593	19.2	4273	11	AK043647	AK043647 Mus muscu
15	588.8	19.0	650	10	BG698525	BG698525 602658855
16	586.6	19.0	593	14	CA308319	CA308319 UI-H-FTL-
17	582	18.8	2250	11	AK050004	AK050004 Mus muscu
18	550.4	17.8	554	14	CA397265	CA397265 cs89a07.y
19	543.2	17.6	688	13	BQ573665	BQ573665 UI-M-FD0-
20	538	17.4	538	14	CB155259	CB155259 K-EST0213
21	516.6	16.7	571	10	AW961995	AW961995 EST374068
22	506.4	16.4	515	12	BM875524	BM875524 1j34a09.y
23	501.8	16.2	1607	11	AK014810	AK014810 Mus muscu
24	497	16.1	497	14	CA395159	CA395159 cs61a04.y
25	482	15.6	566	14	BY704970	BY704970 BY704970
26	479	15.5	571	14	CB615459	CB615459 AMGNNUC:N
27	473.6	15.3	712	12	B1738670	B1738670 603358893
28	469.4	15.2	821	12	B1758291	B1758291 603029943
29	461.6	14.9	743	14	CD354171	CD354171 UI-M-GM0-
30	461	14.9	461	13	BX113721	BX113721 BX113721
31	455.8	14.7	1153	12	BM544206	BM544206 AGENCOURT
32	444.4	14.4	456	12	BM875274	BM875274 1j54a09.x
33	421.8	13.6	573	10	BF045437	BF045437 BP250016B
34	414	13.4	414	14	CA392998	CA392998 cs32b09.y
35	412.6	13.3	603	13	BQ830217	BQ830217 LL61n1072
36	381.6	12.3	474	14	R35320	R35320 YG65a07.r1
37	375	12.1	439	14	R48984	R48984 YG65a07.s1
38	373.6	12.1	807	14	CA316824	CA316824 UI-M-FM0-
39	372.4	12.0	448	14	H51115	H51115 y032c02.s1
40	371.8	12.0	783	13	BQ571565	BQ571565 UI-M-FC0-
41	368.6	11.9	459	9	AW489593	AW489593 UI-M-BH3-
42	359.6	11.6	458	13	BQ829442	BQ829442 LL61n2036
43	357.4	11.6	874	13	BQ894022	BQ894022 AGENCOURT
44	357	11.5	562	10	BE756527	BE756527 210694 MA
45	354.6	11.5	554	10	BF076938	BF076938 226709 MA

ALIGNMENTS

RESULT 1
AK004772
LOCUS
DEFINITION
AK004772 2808 bp mRNA linear HTC 05-DEC-2002
Mus musculus adult male lung cDNA, RIKEN full-length enriched
library, clone:1200014008 product:phosphodiesterase 1B,
Ca2+-calmodulin dependent, 63 kDa, full insert sequence.
ACCESSION
AK004772.1 GI:12836202
VERSION
AK004772.1
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
1
Carninci, P. and Hayashizaki, Y.
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
PUBMED
11042159

REFERENCE AUTHORS	3	Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsuina,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,K., Kira,A. and Hayashizaki,Y. RIKEN Integrated sequence analysis (RISA) system--384-format Genome Res. 10 (11), 1757-1771 (2000)
JOURNAL MEDLINE PUBMED	20530913 11076861	
REFERENCE AUTHORS	4	Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arawaka,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Kochiwa,H., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Balderelli,R., Barish,G., Blake,J., Boffelli,D., Bojunga,N., Carlinici,P., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Lume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Nardone,P., Ring,B., Rindwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyooka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawai,J.H., Kohsuki,S. and Hayashizaki,Y. Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001)
JOURNAL MEDLINE PUBMED	21085660 11217851	
REFERENCE AUTHORS	5	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002)
JOURNAL MEDLINE PUBMED	6 (bases 1 to 2808)	
REFERENCE AUTHORS	6	Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H., Arawaka,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Teijima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y. Direct Submission Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsr.riken.go.jp, url:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
JOURNAL		
TITLE		Please visit our web site (http://genome.gsc.riken.go.jp/) for further details. cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5'-GAGAGAGAGCGCGCAACTCGAGTTTGTATTTTATTTT 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase
COMMENT		


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Db      2479  TTCCCC-----TCCGGGGCCCTGTGGTGGAGGAGATGGGGGGGCTCAGGGC 2533
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Qy      2807  AGGCTCTCTCTGCCCCCAGCTTGGCCCCAGGAAAGCCCAAGTCCAGGTGACTGCCCTCC 2866
Db      2592  AGGCTCC-----TTGGCCCCAGCTCACCCCATTTAAGGCC--AGTCCAGGTGACTG-CCTCC 2645
Qy      2867  TCTTTCTTTGTAATACCAACCATGATGATTTGTACAGTGGGCCCTGTTCATGGGAATCCA 2926
Db      2646  TCTCTCTCTGTAATA-----CATGATTTGTACAGTGGGCCCTGTTCATGGGAATCCA 2700
Qy      2927  CATCCATGCTCTCTAGACCTGTACCCCTGGTACTTCCACCCCTACCCACCCCGAGAAGG 2986
Db      2701  TCTCCATGGTTC-ATTAGACTGCCACTCT----- 2728
Qy      2987  GCAGAGACGATGTGACTACCCCTGCCCTTGGTTTCCAGACCCCTGCTATAGCCAGAG 3046
Db      2729  ---GAACCGCATGTACTCTCCCATGCTCTTGTGCTCTCCAGGCCCTGCTATAGCCAGAG 2785
Qy      3047  AACAAATAAGAAGGAGACACG 3068
Db      2786  ATCAATAAGAAGGAGACCGG 2807

RESULT 2
BI488476 603020977F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5191770 5',
LOCUS mRNA sequence.
DEFINITION BI488476
VERSION BI488476.1 GI:153277704
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 786)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL NIH-MGC http://mgc.nci.nih.gov/
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11479 row: i column: 19
High quality sequence stop: 781.
Location/Qualifiers
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/clone="IMAGE:5191770"
/lab_host="DH10B"
/clone_lib="NIH_MGC_114"
/note="Organ: brain; Vector: pCMV-Sport6; Site:1: NotI;
Site:2: EcoRV (destroyed); RNA source anonymous pool of 6
male brains, age range 23-27 yo. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.5 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 019. Note:
this is a NIH_MGC Library."
BASE COUNT 192 a 223 c 205 g 166 t

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ORIGIN

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Query Match 23.7%; Score 734; DB 12; Length 786;
Best Local Similarity 99.0%; Pred. No. 3.4e-93;
Matches 770; Conservative 0; Mismatches 5; Indels 3; Gaps 3;

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Qy 1093 GACCATGAAGCAGAGCCTTTGCAACAGCTGGAGAGGATTGACAAGCCCAAGAGCCCTGTCTCT 1152
Db 121 GACCATGAAGCAGAGCCTTTGCAACAGCTGGAGAGGATTGACAAGCCCAAGAGCCCTGTCTCT 180
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Qy 1213 GACCAAGGCCCTCATGAGGAGGATTTCTCCGTGAGGTGACAGGAGGAGGATTTGGGCT 1272
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Db 361 CATGCACTTCATTTGGAGCCCAATCTCTGCTGACTGACGTCGAGAGAGAGTTCAGTGG 420
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Db 481 GCCCTCTCTGATGGAAGTGGAGACCCCAACCTCATGCTGACTGTCAGCTTTCGTTCCAC 540
Qy 1513 CTGGGTCAAGCGCATTCAGGAGATAAGCAGAAATGGAAGAACCGGAGCAAGTGGCAT 1572
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Qy 1573 CACCAACAGATGTCATTCAGAGCTGTCCCTCTGTGAAGAGAGGCCGCCATCCCC 1632
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Qy 163: TCCCGAAGATGAACACCAACAGATGGGAATCTGGATTAGCCCTGGGCTGG-CCCAGGT 1691
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RESULT 3
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LOCUS mRNA sequence.
DEFINITION BG390932
ACCESSION BG390932
VERSION BG390932.1 GI:13284380
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 878)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

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TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM10461 row: h column: 02
High quality sequence stop: 688.
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BASE COUNT 202 a 232 c 256 g 188 t
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Query Match 21.5%; Score 665.2; DB 10; Length 878;
Best Local Similarity 96.5%; Pred. No. 1.3e-83;
Matches 745; Conservative 0; Mismatches 18; Indels 9; Gaps 6;
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DB 10 GGGCCAAAGAGGAAGTTGCCCTCTTGGGGCCCTGGGGCTCC- GGGGTCAGGATTTT 69
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QY 152 CACCTCCAGGGCCCATTTCTCAGCTGGCTACAGTGGTGAACAGTGTGAGATGGGGAG 211
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QY 212 ATAAACATGAGGAGCTGAAGAAAATCTGGAGTACACAGCTTCTCTGCTGGAAGCCGTC 271
DB 190 ATAAACATGAGGAGCTGAAGAAAATCTGGAGTACACAGCTTCTCTGCTGGAAGCCGTC 249
QY 272 TACATAGATGAGACAGCGCAATCTTGGACAGGAGGAGAGCTGCAGGAGCTGCGGTCA 331
DB 250 TACATAGATGAGACAGCGCAATCTTGGACAGGAGGAGAGCTGCAGGAGCTGCGGTCA 309
QY 332 GATGCGCTGCTTCGGAGTGGCGGACTGGCTGGCTCCACCTTCACCCAGCAGGCCGCG 391
DB 310 GATGCGCTGCTTCGGAGTGGCGGACTGGCTGGCTCCACCTTCACCCAGCAGGCCGCG 369
QY 392 GCCAAGGCGCGGAGCAGAGAGAGCCCAAGTTCGGAAGCATTGTGCACGCTGTGCAG 451
DB 370 GCCAAGGCGCGGAGCAGAGAGAGCCCAAGTTCGGAAGCATTGTGCACGCTGTGCAG 429
QY 452 GCTGGGATCTTCGTGGAAGCGGATGTTCCGGAGAACATACACCTCTGTGGGCCCC- ACTTA 510
DB 430 GCTGGGATCTTCGTGGAAGCGGATGTTCCGGAGAACATACACCTCTGTGGGCCCCA 489
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QY 571 CTTGAACAGGAGCAGAGATGACCATGCGCTCAGGACCATGTTGTTGAGTTGCTGACTCG 630
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QY 631 GCATACCTCATCAGCCGCTTCAAGATTCCTCCACTGTGTTTGTGATGAGTTTCTCTGGATGC 690
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QY 691 CTTGGAGACAGG--CTATGGGAAGTACAGAATCCTTACCAACAACAGATCCAGG--CA 745
DB 668 CTTGGAGACAGGCTATGGGAAGTACAGAATCCTTACCAACAACAGATCCAGGCA 727
QY 746 GCCGATGTTACCCAGACAGTCATGCTTCTTGTCTCCGACAGGATGCTGC 797
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LOCUS BQ179638 749 bp mRNA linear EST 30-APR-2002
DEFINITION UI-M-EVO-bws-e-08-0-UI.r1 NIH.BMAP_EVO Mus musculus cDNA clone
IMAGE:5701231 5', mRNA sequence.
ACCESSION BQ179638
VERSION BQ179638.1 GI:20355130
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 749)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: Dr. James Lin, University of Iowa
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)
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/clone_lib="NIH_BMAP_EVO"
/note="Organ: brain; Vector: pYX-Asc; Site_1: EcoR I; Site_2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fractionation ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is GTCGCTGGAA. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP). 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institutes of Mental Health (NIMH), Hemlin Chin, Ph.D., program coordinator."
BASE COUNT 183 a 207 c 181 g 178 t
ORIGIN
Query Match 20.8%; Score 643.4; DB 13; Length 749;
Best Local Similarity 91.2%; Pred. No. 1.5e-80;

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Db 1 CCTTGAACCCAGGAGAGATGACCATGCTGAGGACCATGTTTGTGAGTTCGTGACTC 60
QY 630 GGCATACCTCATCAGCCGCTTCAAGATTCCTGAGTTCCTGAGTTCCTGATG 689
Db 61 GGCATACCTCATCAGCCGCTTCAAGATTCCTGAGTTCCTGAGTTCCTGATG 120
QY 690 CCTTGGAGACAGGCTATGGAAGTACAAAGATCCTTACCACAAACAGATCCAGCGCG 749
Db 121 CCTTGGAGACAGGCTATGGAAGTACAAAGATCCTTACCACAAACAGATCCAGCGCG 180
QY 750 ATGTTACCCAGAGAGTCCATTCCTTCTGCTCGCAGGAGTGGTGCATGCTCTCGG 809
Db 181 ACCTGAGCCAGAGTGTCCATTCCTTCTGCTCGCAGGAGTGGTGCATGCTCTCGG 240
QY 810 AGATTGAGCTTCCTGGCCATCATCTTTGCTGAGTATCCATGATGAGCAGCGGCA 869
Db 241 AGATTGAGCTTCCTGGCCATCATCTTTGCTGAGTATCCATGATGAGCAGCGGCA 300
QY 870 CTACCAACAGCTTCCATCCAGACAGTCAAGATGTCGATCGTGTACAATGATCGTT 929
Db 301 CAACCAACAGCTTCCATCCAGACAGTCAAGATGTCGATCGTGTACAATGATCGAT 360
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Db 541 TSCAAGCTGGAGAGATGACAGCCAGCCGCTGCTCTACTGCTCTGCTGCTG 600
QY 1170 ACATCAGCCACCAACAGCAGTGGTGTGTCACAGCGCTGGACCAAGGCCCTCATGG 1229
Db 601 ACATCAGCCACCAACAGCAGTGGTGTGTCACAGCGCTGGACCAAGGCCCTCATGG 660
QY 1230 AGGAATTCCTCCTAGGCTGACAGAGGAGAGTGGCCCTGCTCTCTCCACTCT 1289
Db 661 AGGAATTCCTCCTCCTAGGCTGACAGAGGAGAGTGGCCCTGCTCTCTCCACTCT 720
QY 1290 GTACCCGCACTTCCACTCTAGTGGCCAG 1318
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RESULT 5
B0179626
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
B0179626 737 bp mRNA linear EST 30-APR-2002
UI-M-EV0-bws-c-06-0-01.r1 NIH_BMAP_EV0 Mus musculus CDNA clone
IMAGE:5701181 5', mRNA sequence.
B0179626
B0179626.1 GI:20355118
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cyabps@mail.nih.gov
```

Tissue Procurement: Dr. James Lin, University of Iowa
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

FEATURES

Location/Qualifiers
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/mol_type="mRNA"
/strain="C57BL/6"
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/clone_lib="NIH_BMAP_EV0"
/note="Organ: brain; Vector: pYX-Asc; Site: 1; Ecor I;
Site: 2; Not I; The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured mRNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was size selected according to mRNA size fraction
ligated with Ecor I adaptor, digested with Not I, and then
cloned directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is GTGCGTGA. This library was created for the
University of Iowa Mouse Brain Molecular Anatomy Project
(BMAP). Gene discovered in the Developing Mouse Nervous
System, supported by National Institutes of Mental Health
(NIMH), Hemin Chin, Ph.D., program coordinator."

BASE COUNT

182 a 204 c 176 g 175 t

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Best Local Similarity 91.6%; Pred. No. 1.3e-79;
Matches 674; Conservative 0; Mismatches 62; Indels 0; Gaps 0;
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Db 1 CCTTGAACCCAGGAGAGATGACCATGCTGAGGACCATGTTTGTGAGTTCGTGACTC 60
QY 630 GGCATACCTCATCAGCCGCTTCAAGATTCCTGAGTTCCTGATG 689
Db 61 GGCATACCTCATCAGCCGCTTCAAGATTCCTGAGTTCCTGATG 120
QY 690 CCTTGGAGACAGGCTATGGAAGTACAAAGATCCTTACCACAAACAGATCCAGCGCG 749
Db 121 CCTTGGAGACAGGCTATGGAAGTACAAAGATCCTTACCACAAACAGATCCAGCGCG 180
QY 750 ATGTTACCCAGAGTCCATTCCTTCTGCTCGCAGGAGTGGTGCATGCTCTCGG 809
Db 181 ACCTGAGCCAGAGTGTCCATTCCTTCTGCTCGCAGGAGTGGTGCATGCTCTCGG 240
QY 810 AGATTGAGCTTCCTGGCCATCATCTTTGCTGAGTATCCATGATGAGCAGCGGCA 869
Db 241 AGATTGAGCTTCCTGGCCATCATCTTTGCTGAGTATCCATGATGAGCAGCGGCA 300
QY 870 CTACCAACAGCTTCCATCCAGACAGTCAAGATGTCGATCGTGTACAATGATCGTT 929
Db 301 CAACCAACAGCTTCCATCCAGACAGTCAAGATGTCGATCGTGTACAATGATCGAT 360
QY 930 CAGTGTGGAGATCACCACATCAGCTCTGTTTTCGATGATGAGGATGATGATGA 989
Db 361 CGGTGTGGAGATCACCACATCAGCTCTGTTTTCGATGATGAGGATGATGATGA 420
QY 990 ACATTTTATCACTCACCAGAGTGAATTTGAGAACCTCCAGGCTGGTGTATGAGA 1049
Db 421 ACATTTTATCACTCACCAGAGTGAATTTGAGAACCTCCAGGCTGGTGTATGAGA 480

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QY	215	AACATTGAGAGCTGAAG	AAATCTGGAGTACACAGCTTCTCTGCTGGAAAGCCGCTAC	274
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QY	395	AAAGGCCCGCAGCAG	GAGAGAGCCCAAGTTCGGAAGCATTTGTGCACGCTGTGCAGGCT	454
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Qy	992	ATTTTCATCACTCAACCTCACCAGGATGAGTTTGTAGAAGTCCGAGCCCTGGTTCATTGAGATG	1051
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Qy	1052	GTGTTGGCCACAGACATGCTCTGCCATTTCCAGCAAGTGAAGACCATGAAGACAGACCTTG	1111
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Qy	1112	CAACAGCTGGAGAGGATGACAGAGCCCAAGGCCCTGCTCTACTGCTCCATCTGCTGAC	1171
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Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer
 Genome Res. 10 (11), 1757-1771 (2000)
 20530913
 11076861

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, K., Nishi, K., Kiyosawa, H., Kondo, S., Yamana, I., Saito, T., Okazaki, Y., Gojohori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L. M., Staubli, F., Suzuki, R., Tomita, M., Wagner, J., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazza, R., Mombert, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyooka, K., Wang, K. H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S., and Hayashizaki, Y.

Functional annotation of a full-length mouse cDNA collection

Nature 409 (6821), 685-690 (2001)

21085660

11217851

5

The FANTOM Consortium and the RIKEN Genome Exploration Research

Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases 1 to 2132)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Horii, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission

Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

CDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to

prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.go.jp/

URL: http://fantom.gsc.riken.go.jp/.

Location/Qualifiers

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RESULT 8
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Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 95279253
PUBMED 10345636
REFERENCE
2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,
Sun, N., Ishii, Y., Nakamura, S., Hazama, M., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
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Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsui, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system-384 format
sequencing pipeline with 384 multi-capillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20350913
11076861

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,
Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamana, I.,
Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,
Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,
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Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,
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Toyooka, K., Wang, K. H., Weitz, C., Whittaker, C., Wilming, L.,
Wyshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S.
and Hayashizaki, Y.
Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
21085660
11217851

TITLE
JOURNAL
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AUTHORS

The FANTOM Consortium and the RIKEN Genome Exploration Research
Group phase I & II team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2128)

TITLE
JOURNAL
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REFERENCE
AUTHORS

Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H.,
Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y.,
Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K.,
Hirooka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M.,
Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K.,
Nonura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C.,
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Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K.,
Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
Direct Submission

TITLE
JOURNAL

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URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
Please visit our web site (<http://genome.gsc.riken.go.jp/>) for
further details.

COMMENT

cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken


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full insert sequence.
ACCESSION AK082180
VERSION AK082180.1 GI:26349582
KEYWORDS HIC; CAP trapper.
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 93279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes

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VERSION
HTC: CAP trapper
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Mus musculus (house mouse)
SOURCE
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
REFERENCE
1 Carninci, P., and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
PUBMED
10349636
AUTHORS
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
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JOURNAL

COMMENT

Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
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Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kusunagi, T., Tashiro, H., Itoh, M.,
Sun, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
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sequencing pipeline with 384 multichannel sequencer
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Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,
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Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,
Kakita, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,
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Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N.,
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Ringo, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,
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Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kotsuki, S.,
and Hayashizaki, Y.

Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
21085660
11217851
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The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 4484)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
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Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sugabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takada, Y., Tanaka, T., Tomaru, K., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.

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Kanagawa 230-0045, Japan (E-mail: genome-res@gs.c.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.

Please visit our web site for further details.
URL:<http://genome.gsc.riken.go.jp/>
URL:<http://fantom.gsc.riken.go.jp/>.

FEATURES
SOURCE

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source
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	Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, C., Quackenbush, J., Schriml, L. M., Stauffer, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bul, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Nordone, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mommaerts, P., Sasaki, H., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyo-oka, K., Wang, K. H., Weitz, C., Whitaker, C., Wilming, L., Zukki, S. Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohsaki, S. and Hayashizaki, Y.		/note="putative" 4708. -4713 /note="putative" 4729	
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	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-703 (2002)		Query Match 19.4%; Score 599.6; DB 11; Length 4729; Best Local Similarity 67.9%; Pred. No. 7.7e-75; Matches 85%; Conservative 0; Mismatches 79; Indels 3; Gaps 1;	
TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS	6 (bases 1 to 4729) Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hara, A., Hasegawa, Y., Hashizume, W., Hayashida, K., Hayashizaki, T., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imoto, J., Itoh, M., Kageyama, T., Kasukawa, T., Kato, H., Kikuchi, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koyama, S., Kurahara, C., Matsuyama, T., Miyazaki, A., Murata, M., Okazaki, Y., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Saitoh, K., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.		173 AGCGTCGCTACATGTTGAAGCATGTTGGAGATGGGAGATAAACATGAGCAGCTGAAG 232 118 AGGTTACGCTCTTGTCAAGCAATAGAACAGGAGAGGCGCTCTGTGTGACCTTAAG 177 233 AAAATCTCGAGTACACAGCTCTCTGTGGAGCGCTACATAGATGAGCAGCGCA 292 178 AAGAATCTGGAATATGACGCCACAGCTGTGAATCTGTATATATGATCAACAGGCA 237 293 ATCTTGACACGAGGAGCAGCTGAGAGCTCGGTCAGATGCGCTGCTCGGAGGTG 352 238 CTCTCGATACAGAGATGAGCTTAGTGACATCAATCAGATGCTGTGCTTCAGAGTT 297 353 CGGACTGCTGCGCTCCACCTTCAAGCAGGCGCGGCCCAAGCGCCCGCAGCAGAG 412 298 CGGATGCTGCTGCTCCACCTTCAAGCAGGAGATGATGCTTAGGAGAGTAT 357 413 GAGAAGCCCAAGTTCGAGCATGTTGCGAGCTGGGATCTTCTCGGAGCGG 472 358 GAGAAGCCCAAGTTCGAGCATGTTGCGAGCTGGGATCTTCTCGGAGCGG 417 473 ATGTCGAGAGACATACACCTCTGTGGGCGCCACCTTACTCTACTGCGCTTCTCAACTGT 532 418 ATGTACAGAGGACATCAACATGTTGGGCTGAGCTATCCACCGGCTGTAATCGATGCA 477 533 CTCGAAGACCTGATCTCTGTTGATGCTCTTTTCTTTCCTTGAACAGCAGCAGATGAC 592 478 TTGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 537 593 CATGCTGAGGAGCATTGTTTGTGATGTTGATGTTGATGTTGATGTTGATGTTGATGTTG 652 538 CATGCTGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 597 653 AAGATTCCTGCTGTTTGTGATGTTTGTGATGTTTGTGATGTTTGTGATGTTTGTGATGTT 712 598 AAGATTCCTGCTGTTTGTGATGTTTGTGATGTTTGTGATGTTTGTGATGTTTGTGATGTT 657 713 TACAAGATCTTACCAACACAGATCCACGAGCGGATGTTTACCCAGCAGTCCATGTC 772 658 CACAAAAATCTTACCAACACAGATCCACGAGCGGATGTTTACCCAGCAGTCCATGTC 717	
	Direct Submission Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)			
	CDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.go.jp/ URL: http://phantom.gsc.riken.go.jp/.			
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Qy	1370	ACTGACCTGGCAGAGAGAGTGTTCAGCCCTGCGGATGAGGACTCCAAGTCT	1423
Db	1318	ACGGACATGACCGAGAGATGTTGAGTCCATTAATGACGAAAGCTCCAGACT	1371
RESULT	14		
AK043647			
LOCUS	AK043647	4273 bp	mrna linear HTC 05-DEC-2002
DEFINITION	Mus musculus 10 days neonate cortex cDNA, RIKEN full-length enriched library, clone:A830015G03 product:phosphodiesterase 1A, calmodulin-dependent, full insert sequence.		
ACCESSION	AK043647		
VERSION	AK043647.1	GI:26335810	
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.		
TITLE	High-efficiency full-length cDNA cloning		
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)		
MEDLINE	99279253		
PUBMED	10349636		
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.		
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)		
MEDLINE	20499374		
PUBMED	11042159		
REFERENCE	3		
AUTHORS	Shibata, K., Itoh, M., Alizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Ishiyama, J., Nishi, K., Kitsuina, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Ogawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.		
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer		
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)		
MEDLINE	20530913		
PUBMED	11076861		
AUTHORS	Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Alizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L. M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C., Fietcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyooka, K., Wang, K. H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S., and Hayashizaki, Y.		
TITLE	Functional annotation of a full-length mouse cDNA collection		
JOURNAL	Nature 409 (6821), 685-690 (2001)		
MEDLINE	21085860		
PUBMED	11217851		
AUTHORS	5		
TITLE	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.		
JOURNAL	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs		
REFERENCE	Nature 420, 563-573 (2002)		
AUTHORS	6 (bases 1 to 4273)		
TITLE	Adachi, J., Alizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.		
TITLE	Direct Submission		
JOURNAL	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)		
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.go.jp/ Location/Qualifiers		
FEATURES	1. .4273		
SOURCE			

Job time : 5709 secs

cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LAM10695 row: n column: 14
High quality sequence stop: 648.

FEATURES
source

1. 650
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/clone_lib="NCI_CGAP_Skn3"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
143 a 183 c 173 g 151 t

BASE COUNT
ORIGIN

Query Match 19.0%; Score 588.8; DB 10; Length 650;
Best Local Similarity 99.1%; Pred. No. 6.8e-73;
Matches 634; Conservative 0; Mismatches 2; Indels 4; Gaps 4;
QY 288 GGCAAACTCTTGACACGGAGCAGCTGCAGGAGCTCGGTGCAGATCCCGTTCGG 347
Db 1 GGCAAACTCTTGACACGGAGCAGCTGCAGGAGCTCGGTGCAGATCCCGTTCGG 60
QY 348 AGGTGCGGACTGGTGGCTTCCACCTTCACCCAGCAGCGCCGAGCCGAG 407
Db 61 AGGTGCGGACTGGTGGCTTCCACCTTCACCCAGCAGCGCCGAGCCGAG 120
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QY 528 ACTGTCTCAAGAACCTGGATCTCTGGTCTTGTATGCTTTTCTTGAACACGAGCAGCAG 587
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QY 765 TCCATTGTTCTTGTCTCGGACAGGGA-TGGTGACATGCCCTGTGCGGAGATTGAGCTCCTG 823
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QY 824 GCCATCATCTTGTGTCGACATCCATGATTTAGACACACGGGCACCTACCAACAGCTTC 883
Db 541 GCCATCATCTTGTGTCGACATCCATGATTTAGACACACGGGCACCTACCAACAGCTTC 600
QY 884 CACATCCAGACCAAGTCAGAATGTGCCATCGTGACAAATG 923
Db 601 CACATCCAGACCAAGTCAGAATGTGCCATCGTGACAAATG 640

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